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OM nucleic - nucleic search, using sw model	Run on: October 28, 2003, 15:13:35; Search time 1515 Seconds (without alignments) 270.031 Million cell updates/sec	Title: US-09-335-032-71 Perfect score: 10 Sequence: 1 cttctcttt 10	Scoring table: OLIGO NUC Gapop 60.0 , Gapext 60.0	Searched: 2888711 segs, 20454813386 residues	Word size : 0	Total number of hits satisfying chosen parameters: 5777422	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Listing first 500 summaries	Database: GenEmbl:* 1: gb_ba:* 2: gb_hte:*
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Pred. No. is the number of results predicted by chance to have a

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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Wang, C.-G. and Hepburn, A.G.
Genetic sequence assay using DNA triple strand formation
Patent: US 5861244-A 246 19-JAN-1999;
Location/Qualifiers
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                                               PAT 27-AUG-2002
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                                                                                                            BD065135.1 G1:22610738
P2 2001509017-A/71.
Saccharomyces cerevisiae (baker's yeast)
Saccharomyces cerevisiae
Saccharomyces cerevisiae
Saccharomyces cerevisiae
Saccharomycetales; Saccharomycetales;
1 (bases 1 to 10)
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N JP 2001509017-A/71

PD 10-JUL-2001

PP 22-JAN-1998 JP 1998532117

PR 23-JAN-1997 US 60/035917

PI VICTOR E VELCULESCU JERT VOCELSTEIN, KENNETH W KINZLER PC C12N15/10, C12N15/31, C07K14/395, C12Q1/68, C12Q1/02 CC Characterization of the yeast transcriptome

FT Source | Continuo | 
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Unclassified.

(I (bases I to 12)
Wang,C.-G. and Hepburn,A.G.
Genetic sequence assay using DNA triple strand formation
Patent: US 5861244.A 181 19-JAN-1999;
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.larity 100.0%; Pred. No. 1.5e+05;
Conservative 0; Mismatches 0; Indels
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                                               BD065135 10 bp DNA 1. Characterization of the yeast transcriptome.
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/db_xref="taxon:4932"
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/organism="unknown"
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Zhan, J.
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AX500417/c
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Matches 10; Conservative 0; Mismatches 0; Indels
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Patent: EP 1229046-A 1723 07-AUG-2002;
Aeomica, Inc. (US)
                                       Zhan,J.
Human testis expressed patched like protein
Patent: EP 1229046-A 1721 07-AUG-2002;
Acomica, Inc. (US)
Location/Qualifiers
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Patent: EP 1229046-A 1722 07-AUG-2002;
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100.0%; Pred. No. 1.4e+05;
tive 0; Mismatches 0;
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EP1229046.
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/db_xref="taxon:9606"
                                                                                                                           /organism="Homo sapiens"
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Location/Qualifiers
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Sequence 1723 from Patent
AX500416
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Homo sapiens
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Matches 10; Conservative
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AX500415/c
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Patent: EP 1229046-A 1724 07-AUG-2002;
Aeomica, Inc. (US)
Location/Qualifiers
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100.0%; Pred. No. 1.4e+05;
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Sequence 1725 from Patent BP1229046.
AX500418
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Sequence 1724 from Patent EP1229046.
AX500417
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/mol_type="genomic DNA"
/db_ref="taxon:666"
a 0 c 6 g 3
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/organism="Homo sapiens"
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                   1. .17
/organism="Homo sapiens'
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                             PAT 27-MAR-2003
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                                                                                                                                                                                                                         Telerman, A., Amson, R. and Tuijnder, M. Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and their use as
                                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Matches 10; Conservative 0; Mismatches 0; Indels
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/organism="synthetic construct"
/or__type="genomic DN4"
/db xref="taxon:32630"
/note="oligonucleotide"
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Molecular Engines Laboratories (FR)
Location/Qualifiers
                                                                           AX673153 17 bp DNA Sequence 1598 from Patent WO03004526.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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synthetic construct
artificial sequences.
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AX659410
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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              100.0%; Score 10; DB 6; Length 17; 100.0%; Pred. No. 1.4e+05;
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Human testis expressed patched like protein
Patent: EP 1229046-A 1726 07-AUG-2002;
Aecmica, Inc. (US)
Location/Qualifiers
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Patent: EP 1229046-A 1727 07-AUG-2002;
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                                            0; Mismatches
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Location/Qualifiers
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AX500419.1 GI:23382712
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Query Match
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artificial sequences.

1 (bases 1 to 21)
Yoshioka,T. and Suzuki,R.
Method for detecting Kawasaki disease factor
Patent: JP 200157297-A 83 13-JUN-2000;
SHIONGGI & CO LTD
OS Artificial Sequence
PN JP 2000157297-A/83
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Method for detecting Kawasaki disease factor.
E35992.
JP 2000157297-A/83.
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Minion,F.Chris. and Hsu,T.
Minion,F.Chris. and Hsu,T.
Petcombinant mycoplasma hyopneumoniae vaccine
Patent: US 6162435-A 8 19-DEC-2000;
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C12Q1/68,C12N15/09,G01N33/48,C12N15/00
                                                                             100.0%; Score 10; DB 6; L
100.0%; Pred. No. 1.4e+05;
Live 0; Mismatches 0;
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Sequence 8 from patent US 6162435.
AR136775 GI:14478025
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01-DEC-1998 JP 1998341661
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Location/Qualifiers
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                             /organism="unknown"
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AR136775/c
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                 PAT 12-JUN-2003
                                                                                                                        1 (bases 1 to 20)
Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A., Sankaran,B. and Pletcher,L.D.
Chlamydia pneumoniae polynuclectides and uses thereof
Patent: US 6559294-A 6382 06-MAY-2003;
Location/Qualifiers
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1 (bases 1 to 21)
Gorski, J.
Monitoring an immune response by analysis of amplified immunoglobulin or T-cell-receptor nucleic acid Patent: US 5837447-A 16 17-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [bases 1 to 20]
Gillespie, D. deceased.
Competitor primer asymmetric polymerase chain reaction Patent: US 5627054-A 3 06-MAY-1997;
Location/Qualifiers
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100.0%; Score 10; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 10; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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           20 bp DNA Sequence 6382 from patent US 6559294. AR315845. GI:31709271
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Sequence 16 from patent US 5837447.
AR054595.
AR054595.1 GI:5980172
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Sequence 3 from patent US 5627054.
148976
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Matches 10; Conservative
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Immunostimulatory rna/dna hybrid molecules
Patent: WO 0193902-A 613 13-DEC-2001;
Biosynexus Incorporated (US)
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Immunostimulatory rna/dna hybrid molecules
Patent: WO 0193902-A 614 13-DEC-2001;
Biosynexus Incorporated (US)
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/mol_type="genomic DNA"
/db_xref="texcn:12630"
/note="Synthetic HDR"
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Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 10; Conservative 0; Mismatches 0;
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Sequence 17 from patent US 5891623.
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Sequence 613 from Patent WO0193902.
AX352317
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Sequence 614 from Patent WO0193902.
AX352318
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Synthetic HDR"
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Unclassified.
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1 (bases 1 to 22)
Wang, C.-G. and Hepburn, A.G.
Genetic sequence assay using DNA triple strand formation
Patent: US 5861244-A 65 19-JAN-1999;
Location/Qualifiers
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Immunostimulatory rna/dna hybrid molecules
Patent: WO 0193902-A 612 13-DEC-2001;
Biosynexus Incorporated (US)
Location/Qualifiers
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tive 0; Mismatches 0;
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    /organism="synthetic construct"

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Sequence 65 from patent US 5861244.
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Artificial Sequence
JP 2001321190-A/2633
20-NOV-2001
12-MAN-2001 JP 2001068285
EIICHI SOEDA
CI2NI5/09,CI2N15/09,CI2M1/00,CI2Q1/68,G01N33/53,G01N33/566, PC
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                                                                     Gaps
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Patent: JP 2001321190-A 2633 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
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                                       Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 10; Conservative 0; Mismatches 0; Indels
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Genomics-assisted rapid identification of targets
Patent: WO 0216940-A 46 28-FEB-2002;
Genome Therapeutics Corporation (US)
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 10; Conservative 0; Mismatches 0;
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Sequence 46 from Patent WO0216940.
AX443310. GI:21690705
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A method of arraying genome clo
BD090389.1 GI:22635999
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Dean, R.A. and Wang, Y.-H.

PCR-based method for identifying a fusarium wilt-resistant genotype in plants

Patent: US 6309837-A 3 30-OCT-2001;

Location/Qualifiers

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/organism="unknown"
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Dau, P.C. and Liu, D.
Method of intrafamily fragment analysis of the T cell receptor alpha. and .beta. chain CDR3 regions
Patent: US 6087096-A 16 11-UUL-2000;
Location/Qualifiers
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iive 0; Mismatches 0; Indels
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Sequence 3 from patent US 6309837.
AR175558.1 GI:17916857
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AR17558/c
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AR102693/c
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BASE COUNT ORIGIN

ORGANISM

KEYWORDS

REFERENCE AUTHORS

TITLE

JOURNAL

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JOURNAL FEATURES

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TITLE

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Patent: US 5665355-A 17 09-SEP-1997;
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Matches 10; Conservative
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AX502411/c
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Patent: WO 02072815-A 267 19-SEP-2002;
EIICHI SOEDA, TAKESHI KUKITA
OS Attificial Sequence
PN WO 02072815-A/267
PD 19-SEP-2002
PR 12-MAR-2001 WO 201JP004139
PR 17-MAY-2001 JP 01P 68285
PI EIICHI SOEDA
PC CI2N15/09,C12Q1/68
CC Description of Artificial Sequence: Synthetic DNA FH Location/Qualifiers
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100.0%; Pred. No. 1.3e+05;

    .24
    forganism="synthetic construct"
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/db_xref="taxon:32630"

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/organism="synthetic construct"
/mol type="genomic DNA"
/db_xref="taxon:32630"
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Sequence 17 from patent US 5665355.
164401
164401.1 GI:2481295
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   Location/Qualifiers
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WO 02072815-A/267.
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synthetic construct
artificial sequences.
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BD176467/C
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Score 10; DB 6; Length 24
Best Local Similarity 100.0%; Pred. No. 1.38+05;
Matches 10; Conservative 0; Mismatches 0; Indels
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Patent: EP 1229046-A 3718 07-AUG-2002;
Aeomica, Inc. (US)
Location/Qualifiers
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Human testis expressed patched like protein
Patent: EP 1229946-A 3717 07-AUG-2002;
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Sequence 3718 from Patent EP1229046.
AX502411
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Location/Qualifiers
                                  /organism="unknown"
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Location/Qualifiers
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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larity 100.0%; Pred. No. 1.3e+05;
Conservative 0; Mismatches 0; Indels
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Human testis expressed patched like protein
Patent: EP 1229046-A 3721 07-AUG-2002;
Aeomica, Inc. (US)
Location/Qualifiers
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AX502416
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Sequence 3722 from Patent EP1229046.
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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AX502416/c
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Score 10; DB 6; Length 25
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cive 0; Mismatches 0; Indels
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Patent: EP 1229046-A 3720 07-AUG-2002;
Aeomica, Inc. (US)
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
9 a 2 c 9 g 5
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Location/Qualifiers
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 10; Conservative 0; Mismatches 0; Indels
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Human testis expressed patched like protein
Patent: BP 1229046-A 3727 07-AUG-2002;
Aeomica, Inc. (US)
Location/Qualifiers
           Human testis expressed patched like protein Patent: EP 1229046-A 3725 07-AUG-2002; Aeomica, Inc. (US) Location/Qualifiers
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Sequence 3726 from Patent EP1229046.
AX502419
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/organism="Homo sapiens"
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Location/Qualifiers
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Zhan, J.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                          Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Best Local Similarity 100.0%; Pred. No. 1.3e+05;
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Patent: EP 1229046-A 3723 07-AUG-2002;
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llarity 100.0%; Pred. No. 1.3e+05;
Conservative 0; Mismatches 0;
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Sequence 3724 from Patent EP1229046.
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Sequence 3725 from Patent EP1229046.
AX502418.1 GI:23384711
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/mol_type="genomic DNA"
/db_traxon:9606"
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/mol type="genomic DNA"
/db_xref="taxon:9606"
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Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Human testis expressed patched like protein
Patent: BP 1229046-A 3731 07-AUG-2002;
Aeomica, Inc. (US)
Location/Qualifiers
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/db_xref="taxon:9606"
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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 /mol_type="genomic DNA"
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AJ525492.1 GI:26793728
AJ52492.1 GI:26793728
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                         PAT 27-SEP-2002
                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Arabidopsis thaliana T-DNA flanking sequence, left border, clone
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Sequence 4 from patent US 5627054.
148977.
148977.1 GI:2467440
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/organism="Homo sapiens"
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Matches 10; Conservative
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Direct Submission

Salzergue.S.

Balzergue.S.

Direct Submission

Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue

Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue

Gaston Cremieux, 91057 Evy cedex, FRANCE

PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from

the PCR were directly sequenced from the left or the right border

to determine the genomic sequence flanking the insertion. T-DNA

derived sequences were removed. Information to order the

corresponding mutant line and a link to a database providing a

graphical display of the insertion site are available at

http://dbsgap.versailles.inra.fr/publiclines/. This sequence has

been generated in the framework of the French plant genomics

program 'Genoplante' (http://www.genoplante.com and

http://genoplante-info.infoingen.fr).
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T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites

EMBO Rep. 3 (12), 1152-1157 (2002)
                                                                                               Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, m. and Lecharny, A.

T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites

EMBO Rep. 3 (12), 1152-1157 (2002)
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/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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ive 0; Mismatches 0;
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/cultivar="Wassillewskija"
/db_xref="taxon:3702"
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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AJ525503.1 GI:26793739
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Best Local Similarity 100.

Matches 10; Conservative
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AX040823.1 GI:11340462
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GI:20237526
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synthetic construct
artificial sequences.
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Matches 10; Conserv
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            Direct Submission

Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue gaston Cremieux, 91057 Evry cedex, FRANCE
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobogen.fr).
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Moelling,K.
Inhibition of viruses by antisense oligomers capable of binding to polypurine rich tract of single-stranded RNA or RNA-DNA hybrids Patent: US 5849900-A 23 15-DEC-1998;
                                                                                                                                                                                                                                                                                                                             /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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/organism="Arabidopsis thaliana"
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'note="T-DNA flanking sequence
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/cultivar="Wassillewskija"
/db_xref="taxon:3702"
/clone="098B06"
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AR066258
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Unclassified.

1 (bases 1 to 27)

1 (bases 1 to 27)

2 (bases 1 to 27)

3 (bases 1 to 27)

4 (bases 1 to 27)

5 (bases 2 to 27)

6 (bases 2 to 27)

7 (bases 2 to 27)

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9 (bases 2 to 27)
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Location/Qualifiers
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llarity 100.0%; Pred. No. 1.3e+05;
Conservative 0; Mismatches 0;
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Tribonectins
Patent: WO 0064930-A 16 02-NOV-2000;
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Sequence 962 from Patent WO0129262.
AX115839
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Sequence 16 from Patent WO0064930.
AX040823
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Unclassified.
1 (bases 1 to 33)
Choi,G.H., Kunsch,C.A., Barash,S.C., Dillon,P.J., Dougherty,B.,
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1 (bases 1 to 30)

1 (bases 1 to 30)

Afman, T., Scott, J. and Stanton, L.W.

Compositions and methods of disease diagnosis and therapy

Patent: US 6322976-A 135 27-NOV-2001;

Location/Qualifiers

1.30
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Aitman, T.J., Scott, J. and Stanton, L.W.
Compositions and methods of disease diagnosis and therapy
Patent: US 622976-A 134 27-NOV-2001,
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100.0%; Pred. No. 1.3e+05;
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Sequence 134 from patent US 6322976.
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AR120483.1 GI:14104059
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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AR261657
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AR261656
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                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 29)
Aitman, T.J., Scott, J. and Stanton, L.W.
Compositions and methods of disease diagnosis and therapy
Patent: US 632276-A 133 27-NOV-2001;
Location/Qualifiers
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100.0%; Score 10; DB 6; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 10; Conservative 0; Mismatches 0; Indels
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Sequence 132 from patent US 6322976.
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Sequence 133 from patent US 6322976.
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RHODE ISLAND HOSPITAL (US)
Location/Qualifiers
1. .28
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Earl, W.M., Deborah, D.J., Ming, H., Richard, R.W. and Ana, R.R.
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AX220343
  AUTHORS
TITLE
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1 (Dases 1 to 33)

Kunsch,C.A., Choi,G.H., Johnson,S.L. and Hromockyj,A.

Streptococcus pneumoniae antigens and vaccines

Patent: JP 2001505415-A.246 24-APR-2001;

HUMAN GENOME SCIENCES INC

PD 24-APR-2001

PP 30-OCT-1997 JP 1998520667

PR 31-OCT-1996 US

60/029960

PI CHARLES A KUNSCH,GIL H CHOI,SYDNOR L JOHNSON,ALEX HROMOCKYJ PC

CIRNI,5/31,CI2NS/18,CI2N1/21,C07K14/315,C12Q1/68,A61K39/09, PC
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Streptococcus pneumoniae
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
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100.0%; Pred. No. 1.3e+05;
                                                                                                                 100.0%; Score 10; DB 6; I 100.0%; Pred. No. 1.3e+05; tive 0; Mismatches 0;
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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6
                                                                   /organism="unknown"
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      Fannon, M.R. and Rosen, C.A.
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Key
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B36416
B36416.1 GI:13022642
JP 1999239489-A/3.
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1 (bases 1 to 33)
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Matches 10; Conservative
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BD063492/c
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E36416
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Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Patent: WO 155103-A 3875 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
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/organism='Streptococcus pneumoniae'
Location/Qualifiers
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JP 199239489-A/3
07-SEP-1999
21-OCT-1998 JP 1998338366
21-OCT-1997 US 60/070912
EARL WILLIAM MEI, DEBORAH D JAWASUKI, MING HWANG, PI
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    .33
/organism="Streptococcus pneumoniae"
/mol type="genomic DNA"
/db_xref="taxon:1313"

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100.0%; Pred. No. 1.3e+05;
Live 0; Mismatches 0;
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/db xref="taxon:32630"
Anter JP 1999239489-A 3 07-SEP-1999; SMITHKLINE BEECHAM CORP
S Streptococcus pneumoniae
PN 47 199233489-A/3
PD 07-SEP-1999
PF 21-OCT-1999 UP 1998338366
PR 21-OCT-1997 US 60/070912
PI EARL WILLIAM MEI, DEBORAH D JAWASUKI, PI ANA RISA RENOX
PC C12N15/09, A61K31/00, A61K31/70, A61K38
PC C07K14/315, PC C07K16/12, C12P21/02, G01N33/53//C12P2
PC C07K16/12, C12P21/02, G01N33/53//C12P2
PT SOURCE I. 33
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Sequence 3875 from Patent WO0159103.
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BD182426.1 GI:30793344
WO 02092812-A/1.
synthetic construct
synthetic construct
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I12092.1 GI:909590
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                                                   ORGANISM
                                                                            REFERENCE
AUTHORS
TITLE
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PAT 07-SEP-2001
                                                                                                                   Blatt, L., Mcswiggen, J. and Chowrira, B.M.
Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
Patent: WO 0159103-A 5785 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
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Method and reagent for the inhibition of grid
Method and reagent for the inhibition of grid
Parent: WO 0162911-A 944 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
Location/Qualifiers
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 linear
                                                                                                                                                                                                              1. .38
/organism="synthetic construct"
/orl_type="mRNA"
/db_xref="texcn:32630"
/note="Enzymatic Nucleic Acid"
6 c 13 g 8 t
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100.0%; Score 10; DB 6; I
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 10; Conservative 0; Mismatches 0;
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 mRNA
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AX220343 38 bp n
Sequence 5785 from Patent WO0159103.
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Sequence 944 from Patent WO0162911.
AX273375
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                                         AX220343.1 GI:15548067
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artificial sequences.
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Best Local Similarity
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LOCUS
DEFINITION
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AX273375/c
LOCUS
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KEYWORDS
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ORGANISM
LOCUS
DEFINITION
ACCESSION
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artificial sequences.

E 1 (bases 1 to 40)

Strokew,Y., Tomizuka,K., Yoshida,H. and Ishida,I.
Human artificial chromosomes comprising human artificial
lambda gene, and non-human animals retaining human artificial
chromosome transmittable to progeny
chromosome transmittable to progeny
chromosome transmittable to progeny
RIRIN BREWERY CO LTD, YOSHIMI KUROIWA, KAZUMA TOMIZUKA, HITOSHI
YOSHIDA, ISAO ISHIDA
OS Artificial Sequence
PN WO 02092812-A,I
PD 21-NOV-2002
PP 10-MAY-2002
PP 10-MAY-2001
PP 10-MAY-2001 WO 2002JP004587
PR 11-MAY-2001 JP 01P 143371
PI YOSHIMI KUROIWA, KAZUMA TOMIZUKA, HITOSHI YOSHIDA, ISAO ISHIDA PC
                                                                                                                                                                                                                                                                                                                            10-MAY-2002 WO 2002JP004587

11-MAY-2001 JP 01P 142371

1 YOSHIID KURCHAY, KAZUWA TOMIZUKA, HITOSHI YOSHIDA, ISAO ISHIDA PC

C12N15/09, A01K67/027, CO7K16/00, C12P21/08

Description of Artificial Sequence:primer
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Fisher, C.W., Barnes, H.J. and Estabrook, R.W.
Methods and compositions for the expression of biologically active fusion proteins comprising a eukaryotic cytochrome P450 fused to a reductase in bacteria
Patent: US 5420027-A 33 30-MAY-1995;
Location/Qualifiers
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1 Similarity 100.0%; Score 10; DB 6; Length 42;
1 Similarity 100.0%; Pred. No. 1.2e+05;
10; Conservative 0; Mismarchee
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ilarity 100.0%; Pred. No. 1.2e+05;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers

    .40
    /organism="synthetic construct"
/mol type="genomic DNA"
/db_xref="taxon;32630";

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/organism="unknown"
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Libert Cambers, 91057 Barzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Bry cedex, FRANCE
Gaston Cremieux, 91057 Bry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at thtp://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-inf(http://www.genoplante.com and http://location/Qualifiers
                                                                                                                                                                      Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.

T-DNA integration into the Arabidopsis genome depends on sequences
                                                                                           Eukaryoča; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Unknown.

Unclassified.

1 (bases 1 to 47)

Blumenfeld,M., Chumakov,I., Bougueleret,L. and Cohen,A.

Biallelic markers related to genes involved in drug metabolism Patent: US 6528260-A 765 04-MAR-2003;

Location/Qualifiers

1. 47
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/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/collivar="Wassillewskija"
/db xref="taxon:3702"
/clone="168206"

    .45
/note="T-DNA flanking sequence

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Sequence 765 from patent US 6528260.
                AJ528602.1 GI:26796862
left border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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EMBO Rep. 3 (12), 1152-1157 (2002)
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8
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Balzergue, S.
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Arabidopsis thaliana T-DNA flanking sequence, left border, clone
168E06.
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                                         PAT 16-AUG-2002
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                                                                                                                                                           Candida albicans
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, mitosporic Saccharomycetales, Candida.
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/organism="synthetic construct"
/mol type="genomic DNA"
/db zref="taxon:32630"
/note="oligonucleotide primer ZC12,565"
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    .43
    /organism="Candida albicans"
/mol_type="genomic DNA"
/db_xref="taxon:5476"

                                         AX484623 43 bp DN Sequence 1923 from Patent WO02053728.
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Sequence 8 from Patent W00078978.
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Cohen,D., Chumakov,I. and Blumenfeld,M.

Biallelic markers for use in constructing a high density disequilibrium map of the human genome Patent: US 6537751-A 1546 25-MAR-2003;

Location/Qualifiers
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Cohen,D., Chumakov,I. and Blumenfeld,M.
Biallelic markers for use in constructing a high density disequilibrium map of the human genome
Patent: US 6537751-A 2472 25-WAR-2003;
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Cohen, D., Chumakov, I. and Blumenfeld, M.
Biallelic markers for use in constructing a high density disequilibrium map of the human genome
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Pred. No. 1.2e+05;
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Pred. No. 1.2e+05;
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AR290737
            AR289811 47 bp DNA Sequence 1546 from patent US 6537751.
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Cohen, D., Chumakov, I. and Blumenfeld, M.
Biallelic markers for use in constructing a high density disequilibrium map of the human genome Patent: US 6537751-A 1282 25-MAR-2003;
                                                                                                                                                                                                                                                                                          1 (bases 1 to 47)
Cohen, D., Chumakov, I. and Blumenfeld, M.
Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
Patent: US 637751-A 522 25-MAR-2003;
Location/Qualifiers
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Sequence 522 from patent US 6537751.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Accession number cg29689883"
9 c 2 g 36 t
                                                                 Gaps
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                              Length 50;
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                             100.0%; Score 10; DB 6; L
100.0%; Pred. No. 1.2e+05;
tive 0; Mismatches 0;
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/mol type="genomic DNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Matches 10; Conservative
                              Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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9 c 2 g 35 t
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Dosch, H. Michael.

Methods of controlling T lymphocyte mediated immune responses

Patent: US 6207389-A 37 27-MAR-2001;

Location/Qualifiers
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Nucleic acids containing single nucleotide polymorphisms and methods of use thereof

Patent: WO 0140521-A 1484 07-JUN-2001;

Curagen Corporation (US)

Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/note="Nucleotide deleted between bases 25 and 26
Accession number cg29689883"
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Similarity 100.0%; Pred. No. 1.2e+05;
0; Conservative 0; Mismatches 0;
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Patent: US 6537751-A 3284 25-MAR-2003;
Location/Qualifiers
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Sequence 37 from patent US 6207389.
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42 CTTCTCTTT 33
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41 CTTCTCTTTT 32
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AX158156
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AR139658/c
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Accession number cg43917418"
t 12 c 10 g 23 t
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Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
Patent: W0 0138886-A 757 31-MAY-2001;
Curagen Corporation (US)
Location/Qualifiers
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Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
Patent: WO 0140521-A 3711 07-JUN-2001;
Curagen Corporation [US]
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Accession number cg43917191"
12 c 7 g 20 t
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     100.0%; Score 10; DB 6; I 100.0%; Pred. No. 1.2e+05; tive 0; Mismatches 0;
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Sequence 757 from Patent W00138586.
AX165562
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Homo sapiens
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Best Local Similarity 100.
Matches 10; Conservative
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AX165562
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                        Gaps
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Accession number cg43917418"
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Accession number cg43917418"
16 c 10 g 18 t
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Nucleic acids containing single nucleotide polymorphisms and methods of use thereof.
Patent: W0 0140521-A 3710 07-JUN-2001;
Curagen Corporation (US)
                                                                                                                                                                                                                                                                                                                                        Shimkets, R.A. and Leach, M.

Nucleic acids containing single nucleotide polymorphisms and methods of use thereof

Patent: WO 0140521A 3709 07-JUN-2001;

Curagen Corporation (US)
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     100.0%; Pred. No. 1.2e+05;
tive 0; Mismatches 0; Indels
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WO0140521.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Homo sapiens
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Matches 10; Conservative
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Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue gaston Cremieux, 91057 Evry cedex, FRANCE

PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante.info.infobiogen.fr).
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Arabidopsis thaliana T-DNA flanking sequence, left border, clone
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AJ521150.
AJ521150.1 GI:26789386
AJ521150.1 GI:26789386
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Virialiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, eudicotyledons, core eudicots, rosids, eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                               Brunaud, V., Balzergue, S., Dubreucg, B., Aubourg, S., Samson, F.,
Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,
Lepiniec, L., Caboche, M. and Lecharny, A.
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
DMBO Rep. 3 (12), 1152-1157 (2002)
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/mol type="genomic DNA"
/culfivar="Wassillewskija"
/db xref="texon:3702"
/clone="260A09"
/clone=lib="Arabidopsis thaliana T-DNA insertion lines"
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                    Length 51;
   100.0%; Score 10; DB 6; Length 51
100.0%; Pred. No. 1.2e+05;
Mismatches 0; Indels
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                Query Match 100.
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Matches 10; Conservative
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2 CTTCTCTTT 11
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RESULT 83 AR098682/c

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Location/Qualifiers
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Highly sensitive multimeric nucleic acid probes
Patent: US 6077668-A 41 20-UN-2000;
Location/Qualifiers
                                                                                                       Unclassified.
1 (bases 1 to 53)
Kool, B.T.
Highly sensitive multimeric nucleic acid probes Patent: US 6077668-A 40 20-JUN-2000;
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100.0%; Pred. No. 1.2e+05;
tive 0; Mismatches 0;
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Sequence 40 from patent US 6368802.
Sequence 40 from patent US 6077668. AR098682
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                                              AR098682.1 GI:12808448
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AR204756.1 GI:21502164
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PLN 30-APR-2003
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Arabidopsis thaliana partial mitochondrial small non-messenger RNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (22-JUL-2002) Huttenhofer A., University of Muenster, Institute for Experimental Pathology, Von-Esmarch-Str. 56, 48149 Muenster, GERMANY
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mitochondrion Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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                                                                                              Outcomp. D.T., Jarvis, T. and McSwiggen, J. Stinchcomb. D.T., Jarvis, T. and McSwiggen, J. Nucleic acid based inhibition of CD40 Patent: US 6194150-A 2710 27-FEB-2001; Location/Qualifiers
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100.0%; Pred. No. 1.2e+05;
Live 0; Mismatches 0;
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1. .57
/organism="Arabidopsis thaliana"
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 Sequence 2710 from patent US 6194150.
AR134285
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AJ505724
AJ505724.1 GI:22293620
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/db_xref="taxon:3702"
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Huttenhofer, A.
Direct Submission
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MEDLINE
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                                            6; Length 53;
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Circular DNA vectors for synthesis of RNA and DNA
Patent: US 6368802-A 41 09-APR-2002;
Location/Qualifiers
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Stinchcomb.D.T., Jarvis,T. and McSwiggen,J.
Nucleic acid based inhibition of CD40
Patent: US 6194150-A 2533 27-FEB-2001;
Location/Qualifiers
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Length 61;

PAT 30-NOV-2001

linear

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1
Stefansson,H., Steinthorsdottir,V. and Gulcher,J.R.
Human schlizophrenia gene
Patent: WO 0164876-A 1332 07-SEP-2001;
Decode Genetics EHF. (IS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stefansson, H., Steinthorsdottir, V. and Gulcher, J.R. Human schizophrenia gene Patent: Wo 0164977-A 1332 07-SEP-2001; Decode Genetics EHF. (IS)

Location/Qualifiers
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Sequence 1332 from Patent WO0164877.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                    /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                               Location/Qualifiers
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L Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue gaston Cremieux, 91057 Evry cedex, FRANCE

Gaston Cremieux, 91057 Evry cedex, FRANCE

PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutent line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program "Genoplante" (http://www.genoplante.com and http://genoplante.info.infobogen.fr).
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                                                             PLN 29-MAR-2003
                                                                                                                                        AJ527067.1 GI:26795327

left border; T-DNA flanking sequence.

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                      Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.

T-DNA integration into the Arabidopsis genome depends on sequences
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                           ATH527067 59-MAR-20
Arabidopsis thaliana T-DNA flanking sequence, left border, clone
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100.0%; Pred. No. 1.2e+05;
ive 0; Mismatches 0; Indels
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    .58 / note="T-DNA flanking sequence

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Sequence 1332 from Patent W00164876.
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/cultivar="Wassillewskija"
/db_xref="taxon:3702"
/clone="131H07"
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EMBO Rep. 3 (12), 1152-1157 (2002)
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DELTA BIOTECHNOLOGY LTD (GB); SLEEP DARRELL (GB)
Location/Qualifiers
   Best Local Similarity 100.0%; Pred. No. 1.1e+05; Matches 10; Conservative 0; Mismatches 0;
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Patent: US 6379924-A 1 30-APR-2002;
Location/Qualifiers
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Sequence 1 from patent US 6379924.
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AR207788.1 GI:21507632
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Sequence 5 from patent US 5659122.
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/mol_type="genomic DNA"
/db_rref="taxon:32644"
                                                                                                                                                 70 bp
Sequence 1 from Patent WO9900504.
A81696
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Saccharomycetales; mitosporic Saccharomycetales; Candida.
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Candrida albicans
Bukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales, mitosporic Saccharomycetales, Candida.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Roemer, T., Jiang, B., Boone, C., Bussey, H. and Ohlsen, K.L. Gene disruption methodologies for drug target discovery Patent: WO 02053798-A 2790 11-JUL-2002; Elitra Pharmaceuticals, Inc. (US) Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 10; Conservative 0; Mismatches 0;
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/organism="Candida albicans"
/mol_type="genomic DNA"
/db_xref="taxon:5476"
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Sequence 2790 from Patent W002053728.
AX485490 GI:22319774
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/db_xref="taxon:5476"
6 c 6 g 38 t
/organism="Candida albicans"
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/db_xref="taxon:5476"
22 c 2 g 36 t
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Sequence 152 from Patent WO02053728.
AX482852.
AX482852.1 GI:22317272
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Austin,G.Douglas.
Enhanced expression in plants using non-translated leader sequences
Patent: US 5659122-A 5 19-AUG-1997;
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Vardeddaal,P.J.C.M., van den Berg,I.E.T., Stroobants,A.K., van der
A.D.L., Malingre,H.E.M. and Berger,R.
Direct Submission
Submitted (25-SEP-1997) Department of Metabolic Diseases,
Wilhelmina Children's Hospital, Nieuwe Gracht 137, Utrecht 3512 LK,
The Netherlands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Pases I to 71)
Vredendaal, P.J., van den Berg, I.B., Stroobants, A.K., van der A.D.L., Malingre, H.E. and Berger, R. Stroctural organization of the human short-chain

1-3-hydroxyacyl-Coaladehydrogenase gene
Mamm. Genome 9 (9), 763-768 (1998)
                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens mitochondrial short-chain L-3-hydroxyacyl-CoA dehydrogenase (HADHSC) gene, nuclear gene encoding mitochondrial protein, 5' end of intron 3.

AF026858
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Matches 10; Conservative 0; Mismatches 0; Indels
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/map="4q22-26"
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/gene="HADHSC"
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                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 73)

Edwards,J.B.D.M.; Duclair,E. and Jordan,J.Y.

Edwards,J.B.D.M.; Duclair,E. and Jordan,J.Y.

Patent: JP 2001269182-A 31829 02-OCT-2001;

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Sequence tag and encoded human protein. BD055583
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JP 2001269182-A/31829
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nes 10; Conservative
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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at phase, S phase and G2/M; (2) a method (M2) for screening candidate phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a cyest cell; and (b) monitoring expression of a NORF gene whose expression varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying in cell cycle expression comprising contacting human plan with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1, and (4) a method (M3) for identifying a candidate drug as a candidate drug and monitoring expression in the yeast cell of at least 10 contiguous nucleotides of a NORF gene whose expression is a yeast cell comprising contacting a yeast cell of at least 10 condidate drug and monitoring expression in the yeast cell of at least 10 condidate drug and monitoring expression in the yeast cell of at least 10 condidate drug and monitoring expression in the yeast cell of at least 10 condidate drug and monitoring expression in the yeast cell cycle, the differentially expressed genes may be used as markers of phases of the diffect the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs.

Che pares may be used to study, monitor and affect phases of the cell cycle, the diffect the cell cycle and for identification of antifungal drugs.

Charliage to AAP131261 replace and for identification of the present invention.

Charliage to the expression is
              Yeast transcriptome is encoded by a DNA molecule comprising a yeast

gene involved in cell cycle progression selected from the group of
norannocated ORF (MORF) genes. SAGE (serial analysis gene expression)

tags for highly expressed genes and NORF genes are given in AAV50051 to
AAV50345. The present invention describes: (1) a method of using yeast
genes to modulate the cell cycle which comprises administering to a cell
an isolated DNA molecule comprising a yeast gene which is involved in

cell cycle progression selected from differentially expressed genes
(SAGE tags given in AAV50051 to AAV50345); (2) a method for screening
candidate antifungal drugs which comprises contacting a test substance
with a yeast cell and monitoring expression of a yeast gene which is
involved in cell cycle progression; (3) a method of identifying human
cell cycle progression; (3) a method of identifying human
involved in cell cycle progression; (3) a method of identifying human
cent genes which are involved in cell cycle progression of a yeast gene which is
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                                                                                                                                                                                                                                                                                                      (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                  Vogelstein B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 23; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                               Velculescu VE,
                                                                                                                                                                                               98WO-US01216
                                                                                                                                                                                                                                                   97US-0035917
  Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-427943/36.
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Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle -

Claim 1; Page 23; 419pp; English.

Kinzler K;

Vogelstein B,

Jelculescu V,

WPI; 2001-061874/07

14-JUN-2000; 2000WO-US16223.

21-DEC-2000

99US-0335032

16-JUN-1999;

(UYJO) UNIV JOHNS HOPKINS.

Gaps Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonamnotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds. .; 0 Length 10; Indels Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:660. 100.0%; Score 10; DB 22; 100.0%; Pred. No. 1.8e+04; Sequence 10 BP; 0 A; 3 C; 0 G; 7 T; 0 other; 0; Mismatches BP. AAF33921 standard; DNA; 10 23-MAR-2001 (first entry) Query Match
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Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.

Saccharomyces cerevisiae.

WO200077214-A2.

Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:71.

(first entry)

23-MAR-2001

AAF33332;

AAF33332 standard; DNA; 10 BP

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Matches

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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonamnotated ORF) genes coding sequence of a yeast gene selected from the formulation a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and (2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a cypression varies as in M1, where a test substance which modifies the expression varies as in M1, where a test substance which modifies the expression comprising expression of a NORF gene whose expression comprising contacting human DNA with a probe which comprises of progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1, and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene candidate drug and monitoring expression in the yeast cell with a candidate drug and monitoring expression in the yeast cell with a candidate drug and monitoring spacession in the yeast cell with a genes may be used to study, monitor and affect phases of the cell cycle. The methods may be used to identification of antifungal drugs.

Characterial cycle and for identification of antifungal drugs and monitor and spaces used the cell cycle expression is also used as markers of phases of the cell cycle. The methods may be used to identification of antifungal drugs.

Characterial control of an an expressed of the cell cycle of the cell cycle of the differential drugs. And an expressed of the cell cycle of the cell cycle of the capear in a paracterial of the cell cycle of the capear in a paracterial of the cell cycle of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle -
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Yeast, Saccharomyces cerevisiae, characterisation, cell cycle, NORF, nor previously assigned open reading frame, nonannotated ORF, SAGE, serial analysis of gene expression, antifungal; tag, identification,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonamnotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate and the cell sand (M2) monitoring expression of a NORF gene whose which modifies the expression varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which mose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs nucleotides of a NORF gene whose expression varies of drugs and characteristic effect on gene member of a class of drugs having a characteristic effect on gene candidate drug and monitoring expression in the yeast cell with a candidate drug and monitoring expression in the yeast cell with a candidate drug and monitoring expression in the yeast cell with a candidate drug and monitoring expression in the yeast cell with a candidate drug and monitoring expression in the yeast cell with coll cycle, the cell cycle. The methods may be used as markers of phases of the cell cycle. The methods may be used as markers of phases of the coll cycle, the cell cycle and for identify candidate drugs which harving a marker of a method was a procession of an identify candidate of a method of an identify candidate of a method of an identify candidate of a method was a marker of a deflect the cell cycle.
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the present invention. AAR33262 to AAR33267 represent linkers and PCR
primers used in the SAGE method, in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                  Kinzler K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 398; 419pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF33924 standard; DNA; 10 BP.
                                                                                                                                                                                                                                                                                                                                                                               Vogelstein B,
                                                                                                                                                                                              14-JUN-2000; 2000WO-US16223
                                                                                                                                                                                                                                                         99US-0335032
                                                                                                                                                                                                                                                                                                                 (UYJO ) UNIV JOHNS HOPKINS.
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                  Saccharomyces cerevisiae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-061874/07.
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                                                                             WO200077214-A2.
                                                                                                                                                                                                                                                                                                                                                                               Velculescu V,
                                                                                                                                                                                                                                                            16-JUN-1999;
                                                                                                                                      21-DEC-2000
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X B X B X B X B X

Triple-helix forming region; Triplex formation; DNA detection; identification; bacteria; oncogene; virus; ds. Triple helix forming nucleotides 807-818 of Hepatitis B virus.

Hepatitis B virus.

JS5861244-A. 19-JAN-1999

AAX14794 standard; DNA; 12

24-MAR-1999 (first entry)

4AX14794;

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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonamnotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag, Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression) varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate a cartifungal drugs comprising: (a) contacting a test substance with a cycle system of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene member of a class of drugs having a characteristic effect on gene candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression in a yeast cell comprising contacting a yeast cell comprising contacting a yeast cell comprising contacting a characteristic effect on gene candidate drug and monitoring expression in the yeast cell cycle, the differentially expression may be used as markers of the cell cycle. The methods may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which Apprise the cell cycle, identification of antifungal drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle -
                                                                                        Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.
                                            Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:972.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kinzler K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example; Page 34; 419pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Velculescu V, Vogelstein B,
                                                                                                                                                                                                                                                                                                                                         14-JUN-2000; 2000WO-US16223.
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                                                                                                                                                                                                                                                                                                                                                                                                                                (UYJO ) UNIV JOHNS HOPKINS
  (first entry)
                                                                                                                                                                                                      Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-061874/07.
                                                                                                                                                                                                                                                   WO200077214-A2.
                                                                                                                                                                                                                                                                                                                                                                                     16-JUN-1999;
    23-MAR-2001
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AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
              the present invention. AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present
                                                                                                                                                             Gaps
                                                                                                                                                             0;
                                                                                                                            Length 10;
                                                                                                                                                            Indels
                                                                                                                                                        0;
                                                                                                                      100.0%; Score 10; DB 22;
100.0%; Pred. No. 1.8e+04;
cive 0; Mismatches 0;
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Best Local Similarity 100...
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RESULT 6 AAX14794/c

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Gaps
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0
                                                                                                                                                                                   Triple helix third strand of 23S rRNA gene nucleotides 214-225.
                                                                                                                                                                                                         Triplex formation, DNA detection, triple helix, identification,
  Length 12;
                      Indels
100.0%; Score 10; DB 20; 100.0%; Pred. No. 1.8e+04;
                      0; Mismatches
                                                                                                                                                                                                                     bacteria; oncogene; virus; ss.
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                                                                                                                     AAX14859 standard; DNA; 12
                                                                                                                                                                 (first entry)
          Local Similarity 100.
les 10; Conservative
                                          1 CTICICITIT 10
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                                                      11 CTTCTCTTTT
                                                                                                                                                               24-MAR-1999
                                                                                                                                                                                                                                          Synthetic
                                                                                                                                         AAX14859;
                   Matches
                                                                                               RESULT 7
                                                                                                          AAX14859
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The present sequence represents a potential triple-helix forming region. It can be used to demonstrate the assay of the invention. The assay comprises adding a sample containing double-stranded DNA test sequences, e.g. containing the present sequence, to an aqueous medium containing at least one complex of anchor DNA, attached to a solid support, and reporter DNA, where either a part of the anchor DNA or reporter DNA is designed to form a triple-strand structure with part of the test sequence. Triplex formation results in displacement of the reporter DNA which is detected as an indication of the presence of the DNA test sequence. The method is used to detect DNA sequences, particularly for identification of bacteria (by detecting genes for ribosomal RNA) in clinical samples, but also detection of oncogenes and Hepatitis B virus.

Sequence 12 BP; 8 A; 0 C; 4 G; 0 U; 0 other;

Query Match

Assay of genetic sequences based on triplex formation from double stranded analyte - and hybrid of anchor and reporter sequences, with reporter released if triplex formation occurs, used e.g. to identify

(PROF-) PROFILE DIAGNOSTIC SCI INC.

WPI; 1999-130384/11.

Hepburn AG,

93US-0173489. 93US-0173489. 92US-0968436.

22-DEC-1993; 22-DEC-1993; 29-OCT-1992; Disclosure; Columns 19-20; 168pp; English.

bacteria

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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomers for diagnosis and/or prognosis of cancer and a range of diseases including immune system gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The ABC00010-ABC99989, ABF00010-ABF9989, ABF00010-ABF99989 and ABI00010-ABF99989 and ABI00010-ABF99989 and Specification, where we have detected the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                 This invention describes novel oligonucleotide primers or peptide nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide primer SEQ ID NO 380025 for detecting SNP TSC0063600.
                                                                                                                                                                                                                  of oligonucleotides, useful for diagnosis and cell typing, is igned to detect single nucleotide polymorphisms and cytosine
                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID 267794; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oet or oligonucleotides, useful for diagnosis and cell designed to detect single nucleotide polymorphisms and methylation status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences.
                                                                                                              Berlin K;
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     07-APR-2000; 2000DE-1019173
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                                                                                                            Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Piepenbrock C,
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                                                        (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                              methylation status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clinical samples, but also detection of oncogenes and Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide primer SEQ ID NO 267794 for detecting SNP TSC0000531.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Assay of genetic sequences based on triplex formation from double stranded analyte - and hybrid of anchor and reporter sequences, with reporter released if triplex formation occurs, used e.g. to identify
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Columns 21-22; 168pp; English.
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92US-0968436.
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Best Local Similarity 100.
Matches 10; Conservative
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, entral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99999, ABF0010-ABF9999 ABH00010-ABF9999 and ABI00010-ABF9999 and 
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Sequence 13 BP; 8 A; 0 C; 4 G; 1 T; 0 other;
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RESULT 12

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Homo sapiens.
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                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                   Oligonucleotide SEQ ID NO 53789 for detecting SNP TSC0014813.
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            ABC53772 standard; DNA; 13 BP.
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Best Local Similarity 100.
Marches 10; Conservative
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                                                                                             06-APR-2001; 2001WO-IB00713.
                                                                                                                                          07-APR-2000; 2000DE-1019173.
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nes 10; Conservative
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WO200177384-A2.
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Zhan J;
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                                                                                                                                                          This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE39999, ABF00010-ABF99999, ABH00010-ABH99999 and ABE1001010-ABE392073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                   Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine
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                                                                                                                              Claim 1; SEQ ID 225883; 29pp + Sequence Listing; German.
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Best Local Similarity 100....
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                 WPI; 2001-657177/75.
                                                                                             methylation status
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range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF99989, ABH00010-ABH999899 and
                                                                                                                                                                                              the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1; human testis expressed Patched like protein; testis; adrenal; liver; male germ cell development; bone marrow; brain; kidney; lung; placenta; prostate; skeletal muscle; colon; male infertility; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                               ABIO0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the print specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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2001WO-US00665.
2001WO-US00667.
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30-JAN-2001; 2001WO-US00669.
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Best Local Similarity 100.
Matches 10, Conservative
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30-JAN-2001;
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mapped to human chromosome 10p12.1. HTPL and its coding sequence are useful for diagnosing a disorder caused by mutation in HTPL, and in therapy and manufacture of a medicament for treatment or prevention of such disorder associated with decreased expression or activity of human HTPL. Such disorders include disorders of testis, or adrenal, adult and foetal liver, bone marrow, brain, kidney, lung, placenta, prostate, skeleral muscle or colon function. HTPL proteins and nucleic acids are clinically useful diagnostic markers and potenial therapeutic agents for male infertility and cancer. The present oligonucleotide was used in an example from the invention.
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Sequence 17 BP; 8 A; 0 C; 7 G; 2 T; 0 other;

Gaps ö 100.0%; Score 10; DB 24; Length 17; 100.0%; Pred. No. 1.8e+04; Indels Mismatches ., Conservative 10 α 1 CTICICITII Query Match Best Local Similarity 10; Best Loc Matches 셤

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ABV80475 standard; DNA; 17 BP ABV80475; (first entry) 03-JAN-2003

Human HTPL scanning oligonucleotide SEQ ID 1721.

Human, gene therapy, tumour suppressor, HTPL; chromosome 10p12.1, human testis expressed Patched like protein, testis; adrenal, liver, male germ cell development; bone marrow; brain; kidney; lung; placenta; prostate; skeletal muscle; colon; male infertility; cancer; ss.

Homo sapiens

EP1229046-A2

07-AUG-2002.

28-JAN-2002; 2002EP-0001167

30-JAN-2001; 2001WO-US00663. 30-JAN-2001; 2001WO-US00664. 30-JAN-2001; 2001WO-US00665. 30-JAN-2001; 2001WO-US00667. 30-JAN-2001; 2001WO-US00668. 30-JAN-2001; 2001WO-US00668.

(AEOM-) AEOMICA INC

09-OCT-2001; 2001US-0327898

Zhan J;

WPI; 2002-676582/73.

Novel isolated human testis expressed Patched like protein (HTPL), useful for identifying agonist and antagonist and specific binding partners, and for treating subjects having defects in HTPL -

Example 2; Page 289; 718pp; English.

The present invention relates to human testis expressed Patched like protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL has two isoforms, with a few single base pair differences between the two. One of the single base pair changes introduces a premature stop codon in HTPL-S (§ for short) compared to HTPL-L (L for long). HTPL shares an overall structure organisation with the Patched protein. The shared structural features strongly imply that HTPL plays a role similar ABV80475/C

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to that of Patched, and is a potential tumour suppressor. HTPL is mapped to human chromosome 10p12.1. HTPL and its coding sequence are useful for diagnosing a disorder caused by mutation in HTPL, and in therapy and manufacture of a medicament for treatment or prevention of therapy and manufacture of a medicament for treatment or prevention of HTPL. Such disorder associated with decreased expression or activity of human HTPL. Such disorders include disorders of testis, or adremal, adult and foetal liver, bone marrow, brain, kidney, lung, placenta, prostate, clinically useful diagnostic markers and potenial therapeutic acids are male infertility and cancer. The present oligonucleotide was used in an example from the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, gene therapy, tumour suppressor; HTPL; chromosome 10p12.1;
human testis expressed Patched like protein; testis; adrenal; liver;
male germ cell development; bone marrow; brain; kidney; lung; placenta;
prostate; skeletal muscle; colon; male infertility; cancer; ss.
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30-JAN-2001; 2001WO-US00665.
30-JAN-2001; 2001WO-US00665.
30-JAN-2001; 2001WO-US00668.
30-JAN-2001; 2001WO-US00669.
23-MAY-2001; 2001US-0864761.
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shares an overall structure organisation with the Patched protein. The shared structural features strongly imply that HTPL plays a role similar to that of Patched, and is a potential tumour suppressor. HTPL is important in regulating male germ cell development, and the HTPL gene was mapped to human chromosome 10p12.1. HTPL and its coding sequence are useful for diagnosing a disorder caused by mutation in HTPL, and in therapy and manufacture of a medicament for treatment or prevention of such disorder associated with decreased expression or activity of human HTPL. Such disorders include disorders of testis, or adrenal, adult and foetal liver, bone marrow, brain, kidney, lung, placenta, prostate, skeletal muscle or colon function. HTPL proteins and nucleic acids are clinically useful diagnostic markers and potential therapeutic agents for male infertility and cancer. The present oligonucleotide was used in an example from the invention.
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Sequence 17 BP; 9 A; 0 C; 5 G; 3 T; 0 other;

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Query Match 100.0%; Score 10; DB 24; Length 17; Best Local Similarity 100.0%; Pred. No. 1.8e+04; Matches 10; Conservative 0; Mismatches 0; Indels
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ABV80477 standard; DNA; 17 BP. ABV80477/

(first entry) 03-JAN-2003 ABV80477;

Human HTPL scanning oligonucleotide SEQ ID 1723.

Human; gene therapy, tumour suppressor; HTPL; chromosome 10p12.1; human testis expressed Patched like protein; testis; adrenal; liver; male germ cell development; bone marrow; brain; kidney; lung; placenta; prostate; skeletal muscle; colon; male infertility; cancer; ss.

Homo sapiens.

07-AUG-2002

28-JAN-2002; 2002EP-0001167 30-JAN-2001; 2001WO-US00663.

30-JAN-2001; 2001MO-US00664. 30-JAN-2001; 2001MO-US00665. 30-JAN-2001; 2001MO-US00665. 30-JAN-2001; 2001MO-US00668. 30-JAN-2001; 2001WO-US00669. 23-MAY-2001; 2001US-0864761. 23-MAY-2001; 2001US-0864761 09-OCT-2001; 2001US-0327898

(AEOM-) AEOMICA INC

Zhan J;

WPI; 2002-676582/73.

useful for identifying agonist and antagonist and specific binding partners, and for treating subjects having defects in HTPL -Novel isolated human testis expressed Patched like protein (HTPL),

Example 2; Page 289; 718pp; English.

The present invention relates to human testis expressed Patched like protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL has two isoforms, with a few single base pair differences between the

The present invention relates to human testis expressed Patched like

Example 2; Page 289; 718pp; English.

Novel isolated human testis expressed Patched like protein (HTPL), useful for identifying agonist and antagonist and specific binding partners, and for treating subjects having defects in HTPL -

WPI; 2002-676582/73.

two. One of the single base pair changes introduces a premature stop codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL shared are an overall structure organisation with the Patched protein. The shared structural features strongly imply that HTPL plays a role similar to that of Patched, and is a potential tumour suppressor. HTPL is important in regulating male germ cell development, and the HTPL gene was mapped to human chromosome 10pl2.1. HTPL and its coding sequence are useful for diagnosing a disorder caused by mutation in HTPL, and in therapy and manufacture of a medicament for treatment or prevention of such disorder associated with decreased expression or activity of human HTPL. Such disorders include disorders of testis, or adrenal, adult and foetal liver, bone marrow, brain, kidney, lung, placenta, prostate, skeletal muscle or colon function. HTPL proteins and nucleic acids are clinically useful diagnostic markers and potenial therapeutic agents for male infertility and cancer. The present oligonucleotide was used in an Human, gene therapy; tumour suppressor; HTPL; chromosome 10p12.1; human testis expressed Patched like protein, testis; adrenal; liver; male germ cell development; bone marrow; brain; kidney; lung; placenta; prostate; skeletal muscle; colon; male infertility; cancer; ss. 0; Gaps 100.0%; Score 10; DB 24; Length 17; 100.0%; Pred. No. 1.8e+04; ive 0; Mismatches 0; Indels Human HTPL scanning oligonucleotide SEQ ID 1724. Sequence 17 BP; 8 A; 0 C; 6 G; 3 T; 0 other; ABV80478 standard; DNA; 17 BP. 2001WO-US00664. 2001WO-US00665. 2001WO-US00667. 30-JAN-2001; 2001WO-US00669. 23-MAY-2001; 2001US-0864761. 28-JAN-2002; 2002EP-0001167. 30-JAN-2001; 2001WO-US00668 09-OCT-2001; 2001US-0327898 example from the invention. 03-JAN-2003 (first entry) Query Match Best Local Similarity 100. Matches 10, Conservative 1 CTTCTCTTTT 10 14 CTÍCTCTTTT 5 (AEOM-) AEOMICA INC 30-JAN-2001; 2 30-JAN-2001; 2 30-JAN-2001; 2 Homo sapiens. EP1229046-A2. 30-JAN-2001; 07-AUG-2002 ABV80478; Zhan J; ABV80478/c RESULT 20 88888888888888888888888 g à

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protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL has two isoforms, with a few single base pair differences between the two. One of the single base pair changes introduces a premeture stop codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL shares an overall structure organisation with the Patched protein. The shares an overall strongly imply that HTPL plays a role similar to that of Patched, and is a potential tumour suppressor. HTPL is important in regulating male germ cell development, and the HTPL gene was imposed to human chromosome lopiz. HTPL and its coding sequence are useful for diagnosing a disorder caused by mutation in HTPL, and in therapy and manufacture of a medicament for treatment or prevention of such disorder associated with decreased expression or activity of human HTPL. Such disorders include disorders of testis, or adrenal, adult and foetal liver, bone marrow, brain, kidney, lung, placenta, prostate, shelteral muscle or colon function. HTPL proteins and nucleic acids are clinically useful diagnostic markers and potenial therapeutic agents for male infertility and cancer. The present oligonucleotide was used in an example from the invention.
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Sequence 17 BP; 8 A; 0 C; 6 G; 3 T; 0 other;

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Gaps
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100.0%; Score 10; DB 24; Length 17; 100.0%; Pred. No. 1.8e+04; tive 0; Mismatches 0; Indels
             Local Similarity 100.
                                                         1 CTTCTCTTT 10
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Human HTPL scanning oligonucleotide SEQ ID 1725. ABV80479 standard; DNA; 17 03-JAN-2003 (first entry) ABV80479; RESULT 21

Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1; human testis expressed Patched like protein; testis; adrenal; liver; male germ cell development; bone marrow; brain; kidney; lung; placenta; prostate; skeletal muscle; colon; male infertility; cancer; ss.

Homo sapiens.

EP1229046-A2 07-AUG-2002. 28-JAN-2002; 2002EP-0001167

30-JAN-2001; 2001WO-US00663. 30-JAN-2001; 2001WO-US00664. 30-JAN-2001; 2001WO-US00665. 30-JAN-2001; 2001WO-US00667. 30-JAN-2001; 2001WO-US00669. 23-MAY-2001; 2001WO-US00669. 09-OCT-2001; 2001US-0B64761.

(AEOM-.) AEOMICA INC

Zhan J;

WPI; 2002-676582/73.

Novel isolated human testis expressed Patched like protein (HTPL), useful for identifying agonist and antagonist and specific binding partners, and for treating subjects having defects in HTPL -

Example 2; Page 290; 718pp; English

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The present invention relates to human testis expressed Patched like protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL has two isoforms, with a few single base pair differences between the two one of the single base pair changes introduces a premature stop codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL context and vertical structure organisation with the Patched protein. The context are structured features strongly imply that HTPL plays a role similar to that of Patched, and is a potential tumour suppressor. HTPL is important in regulating male germ cell development, and the HTPL gene was mapped to human chromosome loppin. HTPL and its coding sequence are useful for diagnosing a disorder caused by mutation in HTPL, and in therapy and manufacture of a medicament for treatment or prevention of therapy and manufacture of a medicament for treatment or prevention of therapy and manufacture of a medicament for treatment or prevention of therapy and manufacture which decreased expression or activity of human HTPL. Such disorders include disorders of lung, placenta, prostate, skeletal muscle or colon, function. HTPL proteins and nucleic acids are clinically useful diagnostic markers and potenial therapeutic agents for male infertility and cancer. The present oligonucleotide was used in an antice example from the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, gene therapy, tumour suppressor; HTPL; chromosome 10p12.1; human testis expressed Patched like protein; testis; adrenal; liver; male germ cell development; bone marrow; brain; kidney; lung; placenta; prostate; skeletal muscle; colon; male infertility; cancer; ss.
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30-JAN-2001; 2001W0-US00665.
30-JAN-2001; 2001W0-US00667.
30-JAN-2001; 2001W0-US00669.
33-JAN-2001; 2001W0-US00669.
23-MAY-2001; 2001US-0864761.
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The present invention relates to human testis expressed Patched like protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL has two isoforms, with a few single base pair differences between the two. One of the single base pair changes introduces a premature stop codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL shares an overall structure organisation with the Patched protein. The shares an overall structure organisation with the Patched protein. The chart of Patched, and is a potential tumour suppressor. HTPL gene was important in regulating male germ cell development, and the HTPL gene was important in regulating male germ cell development, and the HTPL gene was important in regulating male germ cell development or prevention of seeful for diagnosing a disorder caused by mutation in HTPL, and in therapy and manufacture of a medicament for treatment or prevention of such disorders associated with decreased expression or activity of human HTPL. Such disorders include disorders of testis, or adrenal, adult and foetal liver, bone marrow, brain, kidney, lung, placenta, prostate, skelletal muscle or colon function. HTPL proteins and nucleic acids are clinically useful diagnostic markers and potenial therapeutic agents for male infertility and cancer. The present oligonucleotide was used in an example from the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1; human testis expressed Parched like protein; testis; adrenal; liver; male germ cell development; bone marrow; brain; kidney; lung; placenta; prostate; skeletal muscle; colon; male infertility; cancer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence 17 BP; 8 A; 1 C; 4 G; 4 T; 0 other;
                 Example 2; Page 290; 718pp; English.
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09-OCT-2001; 2001US-0327898.
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Best Local Similarity 100.0
Matches 10; Conservative
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The present invention relates to human testis expressed Patched like protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL has two isoforms, with a few single base pair differences between the two. One of the single base pair changes introduces a premature stop codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL shares an overall structure organisation with the Patched protein. The shares an overall structure strongly imply that HTPL plays a role similar to that of Patched, and is a potential tumour suppressor. HTPL gene was important in regulating male germ cell development, and the HTPL gene was mapped to human chromsome 10p12.1. HTPL and its coding sequence are useful for diagnosing a disorder caused by mutation in HTPL, and in therapy and manufacture of a medicament for treatment or prevention of such disorder associated with decreased expression or activity of human HTPL. Such disorders include disorders of testis, or adrenal, adult and fortal liver, bone marrow, brain, kidney, lung, placenta, prostate, skeleal muscle or colon function. HTPL proteins and nucleic acids are clinically useful diagnostic markers and potenial therapeutic agents for male infertility and cancer. The present oligonucleotide was used in an example from the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAPP-E; human; pregnancy associated plasma protein E; abortive; contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis; dysgenetic pregnancy; primer; ss.
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useful for identifying agonist and antagonist and specific binding partners, and for treating subjects having defects in HTPL -
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                                                         Example 2; Page 290; 718pp; English.
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Gaps

This invention describes a novel isolated nucleic acid that encodes

associated plasma protein E, for preventing or aborting pregnancy New isolated nucleic acid encoding an isoform of human pregnancy

WPI; 2002-697817/75.

Example 2; Page 113; 353pp; English.

Sequence 17 BP; 10 A; 2 C; 4 G; 1 T; 0 other;

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one of three new isoforms of human pregnancy associated plasma protein E, activity and can be used for gene therapy or in a vaccine. The nucleic acid, polypeptide encoded by it, or antibody to the polypeptide can be used in pharmaceutical compositions or vaccines for preventing or used in pharmaceutical compositions or vaccines for preventing or dysgenetic pregnancy. PAPP-E is used in the antenatal diagnosis of dysgenetic pregnancies. The nucleic acids are used as probes to assess the level of PAPP-E isoform mRNA in chorionic villus samples, and the proteins in chorionic villus samples, and the proteins in chorionic villus samples, to diagnose dysgenetic pregnancies multipodies can be used to assess the expression levels of PAPP-E isoform proteins in chorionic villus samples, to diagnose dysgenetic pregnancies antenatally. This sequence reperseents an oligomer used in scanning the human PAPP-E genes described in the disclosure of the invention.
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100.0%; Score 10; DB 24; Length 17; 100.0%; Pred. No. 1.8e+04;
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                                    Mismatches
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Query Match
Best Local Similarity 100.
Matches 10; Conservative
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Gaps

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ABS74762/c ID ABS74762 standard; DNA; 17 BP. 24-DEC-2002 ABS74762; RESULT 25

(first entry)

Human PAPP-Ea associated 17-mer SEQ ID 288.

PAPP-E; human; pregnancy associated plasma protein E; abortive; contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis; dysgenetic pregnancy; primer; ss.

Homo sapiens

US2002102252-Al

01-AUG-2002.

06-APR-2001; 2001US-0827998

26-MAY-2000; 2000US-207456P

(GUYY/) GU Y. (SHAN/) SHANNON M E.

Gu Y, Shannon ME;

WPI; 2002-697817/75.

New isolated nucleic acid encoding an isoform of human pregnancy associated plasma protein E, for preventing or aborting pregnancy

Example 2; Page 113; 353pp; English

one of three new isoforms of human pregnancy associated plasma protein E. ApkPP-E. The products of the invention have abortive and contradeptive activity and can be used for gene therapy or in a vaccine. The nucleic acid, polypeptide encoded by it, or antibody to the polypeptide can be aborting pregnancy. PAPP-E is used in the antenatal diagnosis of dysgenetic pregnancies. The nucleic acids are used as probes to assess the level of PAPP-E isoform MRNA in chorionic villus samples, and the antibodies can be used to assess the expression levels of PAPP-E isoform mRNA in chorionic villus samples, and the proteins in chorionic villus samples, to diagnose dysgenetic pregnancies antenatally. This sequence reperseents an oligomer used in scanning the human PAPP-E genes described in the disclosure of the invention. This invention describes a novel isolated nucleic acid that encodes

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Gaps

0;

100.0%; Score 10; DB 24; Length 17; 100.0%; Pred. No. 1.8e+04; tive 0; Mismatches 0; Indels

Query Match
Best Local Similarity 100.
Matches 10; Conservative

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1 CTTCTCTTTT 15 CTTCTCTTT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  one of three new isoforms of human pregnancy associated plasma protein E, healthire. The products of the invention have abortive and contradeptive activity and can be used for gene therapy or in a vaccine. The nucleic acid, polypeptide encoded by it, or antibody to the polypeptide can be aborting pregnancy. PAPPE is used in the antenatal diagnosis of dysgenetic pregnancies. The nucleic ace used as probes to assess the level of PAPPE isoform mRNA in chorionic villus samples, and the antibodies can be used to assess the expression levels of PAPPE isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteins in chorionic villus samples, to diagnose dysgenetic pregnancies antenatally. This sequence represents an oligomer used in scanning the human PAPP-E genes described in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                  PAPP-E; human; pregnancy associated plasma protein E; abortive; contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis; dysgenetic pregnancy; primer; ss.
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel isolated nucleic acid that encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid encoding an isoform of human pregnancy associated plasma protein E, for preventing or aborting pregnancy
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      Length 17;
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100.0%; Score 10; DB 24;
100.0%; Pred. No. 1.8e+04;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                     Human PAPP-Ea associated 17-mer SEQ ID 289.
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ID ABS74763 standard; DNA; 17 BP.
              100.08;
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              Best_Local Similarity 100.
Matches 10; Conservative
                                                             1 CTTCTCTTT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GUYY/) GU Y.
(SHAN/) SHANNON M E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-697817/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shannon ME;
                                                                                                                                                                                                                                                                                                                                                                                                  US2002102252-A1
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                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                        ABS74763;
Query Match
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RESULT 27

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This invention describes a novel isolated nucleic acid that encodes one of three new isoforms of human pregnancy associated plasma protein E, hPAPP-E. The products of the invention have abortive and contraceptive activity and can be used for gene therapy or in a vaccine. The nucleic acid, polypeptide encoded by it, or antibody to the polypeptide can be used in pharmaceutical compositions or vaccines for preventing or aborting pregnancy. PAPP-E is used in the antenatal diagnosis of dysgenetic pregnancies. The nucleic acids are used as probes to assess the level of PAPP-E isoform mRNA in chorionic villus samples, and the antibodies can be used to assess the expression levels of PAPP-E isoform antibodies can be used to assess the expression levels of PAPP-E isoform proteins in chorionic villus samples, to diagnose dysgenetic pregnancies antenatally. This sequence reperseents an oligomer used in scanning the human PAPP-E genes described in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAPP-E; human; pregnancy associated plasma protein E; abortive; contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
                                                                                                                                                   PAPP-E; human; pregnancy associated plasma protein E; abortive; contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis; dysgenetic pregnancy; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid encoding an isoform of human pregnancy associated plasma protein E, for preventing or aborting pregnancy
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100.0%; Pred. No. 1.8e+04;
cive 0; Mismatches 0;
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                                                                                                                    Human PAPP-Ea associated 17-mer SEQ ID 290.
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                BP
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                ABS74764 standard; DNA; 17
                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shannon ME;
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ABS74764/c
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Gaps

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This invention describes a novel isolated nucleic acid that encodes one of three new isoforms of human pregnancy associated plasma protein E, PPAPP-E. The products of the invention have abortive and contraceptive activity and can be used for gene therapy or in a vaccine. The nucleic acid, polypeptide encoded by it, or antibody to the polypeptide can be used in pharmaceutical compositions or vaccines for preventing or aborting pregnancy. PAPP-E is used in the antenatal diagnosis of dysgenetic pregnancies. The nucleic acids are used as probes to assess the level of PAPP-E isoform mRNA in chorionic villus samples, and the artibodies can be used to assess the expression levels of PAPP-E isoform proteins in chorionic villus samples, to diagnose dysgenetic pregnancies antenatally. This sequence reperseents an oligomer used in scanning the human PAPP-E genes described in the disclosure of the invention.
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                                                                                                                                                                                                                                                                                                                 associated plasma protein E, for preventing or aborting pregnancy
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   SS.
dysgenetic pregnancy; primer;
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ses 10; Conservative
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                                                              US2002102252-A1
                                Homo sapiens.
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New isolated nucleic acid encoding an isoform of human pregnancy associated plasma protein E, for preventing or aborting pregnancy
                                                               New isolated nucleic acid encoding an isoform of human pregnancy associated plasma protein E, for preventing or aborting pregnancy
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                                                                                                                                                                                                                                                Sequence 17 BP; 10 A; 1 C; 4 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Human PAPP-Ea associated 17-mer SEQ ID 293.
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                                                                                            Example 2; Page 113; 353pp; English.
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                                                                                                                                                                                                                                                                                                         1 CTTCTCTTTT 10
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          SHANNON M E
                                              WPI; 2002-697817/75
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                            Shannon ME;
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(GUYY/) GU Y.
(SHAN/) SHANN
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invention describes a novel isolated nucleic acid that encodes
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(SHAN/) SHANNON M E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 CTTCTCTTT
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                                                                                                                                                                                                                                                                                                                                               one of three new isoforms of human pregnancy associated plasma protein E, activity and can be used for gene therapy or in a vaccine. The nucleic acid, polypeptide encoded by it, or antibody to the polypeptide can be used in pharmaceutical compositions or vaccines for preventing or aborting pregnancy. PAPP-E is used in the antenatal diagnosis of dysgenetic pregnancies. The nucleic acids are used as probes to assess the level of papp-E isoform mRNA in chorionic villus samples, and the antibodies can be used to assess the expression levels of PAPP-E isoform mRNA in chorionic villus samples, and the antibodies can be used to assess the expression levels of PAPP-E isoform pretains in chorionic villus samples, to diagnose dysgenetic pregnancies antibodies. This sequence repersents an oligomer used in scanning the human PAPP-E genes described in the disclosure of the invention.
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ö This invention describes a novel isolated mucleic acid that encodes one of three new isoforms of human pregnancy associated plasma protein E, MPAPP-E. The products of the invention have abortive and contraceptive activity and can be used for gene therapy or in a vaccine. The nucleic acid, polypeptide encoded by it, or antibody to the polypeptide can be used in pharmaceutical compositions or vaccines for preventing or aborting pregnancy. PAPP-E is used in the antenatal diagnosis of dysgenetic pregnancies. The nucleic acids are used as probes to assess the level of PAPP-E isoform mRNA in chorionic villus samples, and the antibodies can be used to assess the expression levels of PAPP-E isoform proteins in chorionic villus samples, to diagnose dysgenetic pregnancies antenatally. This sequence represents an oligomer used in scanning the one of three new isoforms of human pregnancy associated plasma protein E, hPAPP-E. The products of the invention have abortive and contraceptive activity and can be used for gene therapy or in a vaccine. The nucleic acid, polypeptide encoded by it, or antibody to the polypeptide can be used in pharmaceutical compositions or vaccines for preventing or aborting pregnancy. PAPP-E is used in the antenatal diagnosis of dysgenetic pregnancies. The nucleic acids are used as probes to assess the level of PAPP-E isoform MRNA in chorionic villus samples, and the antibodies can be used to assess the expression levels of PAPP-E isoform proteins in chorionic villus samples, to diagnose dysgenetic pregnancies antenatally. This sequence represents an oligomer used in scanning the human PAPP-E genes described in the disclosure of the invention. PAPP-E; human; pregnancy associated plasma protein E; abortive; contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis; Gaps New isolated nucleic acid encoding an isoform of human pregnancy associated plasma protein E, for preventing or aborting pregnancy . 0 .match 100.0%; Score 10; DB 24; Length 17; Local Similarity 100.0%; Pred. No. 1.8e+04; les 10; Conservative 0; Mismatchee Sequence 17 BP; 10 A; 0 C; 4 G; 3 T; 0 other; Human PAPP-Ea associated 17-mer SEQ ID 294. Example 2; Page 113; 353pp; English. dysgenetic pregnancy; primer; ss. ABS74768 standard; DNA; 17 BP. 26-MAY-2000; 2000US-207456P. 06-APR-2001; 2001US-0827998. 24-DEC-2002 (first entry)

Asymmetric polymerase chain reaction; nucleic acid amplification; PCR; detection; assay; exfoliative toxin A; ETA; skin lesion; competitive primer; capture probe; ss.

96US-0628417. 9605-0628417.

05-APR-1996; 05-APR-1996;

06-MAY-1997. US5627054-A. Synthetic.

(USSA) US SEC OF ARMY.

Staphylococcus aureus exfoliative toxin A gene PCR primer ETA-B.

AAT76779 standard; DNA; 20 BP.

4 CTTCTCTTT 13

15-SEP-1997 (first entry)

AAT76779;

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RESULT 33
                                                                             AAT76779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes novel oligonucleotide probes used to detect contaminant bacteria that may be present in drinking water. The probes can detect bacteria (especially legionella, faecal streptococci and coliforms) that may contaminate drinking water in environmental samples (water or soil), clinical samples (sputum, biopsies, urine etc.), in bathing and drinking water and in foods, pharmaceuticals and cosmetics, by in situ hybridisation. The probes combine the advantages of fluorescent in situ hybridisation with those of culture methods. Only a relatively short culture step is required, analysis takes 24-48 hours (contrast many days for conventional methods) and all relevant bacteria can be tested simultaneously. The oligonucleotides can differentiate between species of the same genus and are easy to use, allowing simple analysis of a large number of samples. ABX94532-ABX94578 represent the
                                                                                                                                                                                                                                                                                                                                                                                                                                                Detection, probe, contaminant, drinking water, Legionella, coliform, faecal streptococci, soil; sputum, biopsy, urine, food, pharmaceutical, cosmetic, fluorescent in situ hybridisation, FISH, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New oligonucleotides, useful for detecting bacteria that may contaminate drinking water, provide quick results for many species in
                                                                                                                    Gaps
  human PAPP-E genes described in the disclosure of the invention.
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                                                                             100.0%; Score 10; DB 24; Length 17; 100.0%; Pred. No. 1.8e+04;
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oligonucleotide probes described in the invention.
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                                      Sequence 17 BP; 9 A; 1 C; 4 G; 3 T; 0 other;
                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           23S/16S rRNA detecting probe SEQ ID 12.
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                                                                                                                                                                                                                                                                                           ABX94543 standard; DNA; 19 BP.
                                                                                             Sest Local Similarity 100.0%;
Matches 10; Conservative (
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11-DEC-2001; 2001DE-1060666.
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                                                                                                                                                      1 CITCICITIT 10
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                                                                                                                                                                                             10 CTTCTCTTT 1
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Quantitative nucleic acid amplification - by competitor primer

asymmetric polymerase chain reaction Example 1; Column 5; 9pp; English.

WPI; 1997-271311/24.

Gillespie D;

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Known or unknown) of a double-stranded nucleic acid segment to produce single-stranded nucleic acid, the Apportional to the single-stranded nucleic acid, the Staphylococcus aureus tarting amount of the nucleic acid, the Staphylococcus aureus extenting amount of the nucleoides 165-436 was amplified by symmetric, exfoliative toxin A (ETA) gene was used as the DNA template. The region comprising nucleotides 165-436 was amplified by symmetric, asymmetric or competitor primer symmetric PCR using the primers ETA-A2 and ETA-B was reduced and for competitor primer asymmetric or asymmetric or competitor primer ETA-A2 after the initial cycling reaction. PCR with upstream primer ETA-A2 after the initial cycling reaction. PCR products containing ETA-specific sequences were detected radioactively by a capture system which employed a bifunctional council to acopture home probe ETA-CP (see AAT76781 and AAT76782). ETA-CP was designed to capture probe ETA-CP (see AAT76781 and AAT76782). ETA-CP was designed controlled and acopture membranes. A radioactively labelled "label probe" (see AAT76783), complementary to nucleotides 389-410 of the ETA gene and through hybridisation of the complementary to nucleotides 389-410 of the ETA gene was used to complementary to nucleotides 389-410 of the ETA gene was used to capture probe and label probe to the denatured symmetric PCR single-stranded PCR product was much less efficient than hybridisation to the capture contains and competitor asymmetric and competitor
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Matches 10; Conservative
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100.0%; Pred. ...

Best Local Similarity 100. Matches 10; Conservative

Query Match

1 CITCTCTTT 10

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100.0%; Score 10; DB 25; Length 19; 100.0%; Pred. No. 1.8e+04;

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dingle nuclectide polymorphism. Minimarch, interaction disease, cardiovascular disease, infectious disease, tumour; metabolic disease, cardiovascular disease, infectious disease, immunological disease, HIV, central nervous system disease, wound healing, chemotherapy side effect, anaemia, osteoporosis, gastrointestinal disease, veneral disease, AIDS, obesity, hepatitis, infectious pneumonia, Alzheimer's disease, allergy, Parkinson's disease, multiple sclerosis, schizophrenia, depression, graft versus host disease, asthma; psoriasis, rheumatoid arthritis, crohn's disease, ulcerative colitis; genital wart; sequencing; primer.
                                                                                                                                                                                                                                                                                                                                                                                                                 AAX91991-X97517 represent PCR primers used to amplify open reading frames and other nucleic acid sequences from the genome of chlamydia pneumoniae (see AAX91990). C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent by the open reading frames of the C. pneumoniae genome (see AAY94584-AAY35879) can be used in immunogenic compositions as vaccines. Vectors immunogenic compositions, especially where the vector directs the
              Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; ss; cellular proliferation inhibitor; interferon alpha 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression of a neutralising epitope of C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 10; DB 20; 100.0%; Pred. No. 1.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human interferon alpha 2 sequencing primer #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 BP; 8 A; 4 C; 4 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                        Genome sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                       Page 1874; Disclosure; 1912pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAL51617 standard; DNA; 20 BP.
                                                                                                                                                                                                                    98US-0107078.
97FR-0014673.
                                                                                                                                                                                       98WO-IB01890,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10
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                                                                                          Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                             WPI; 1999-357842/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 CTTCTCTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CTTCTCTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                               (GEST ) GENSET
                                                                                                                       WO9927105-A2
                                                                                                                                                                                   20-NOV-1998;
                                                                                                                                                                                                                    04-NOV-1998;
                                                                                                                                                                                                                                    21-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                        03-JUN-1999
                                                                                                                                                                                                                                                                                              Griffais R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAL51617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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AAL51617/c
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                                                                                                                                                                                          paratrachoma, inclusion conjunctivitis; genital disease, perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; PCR primer; bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs encode polypeptides (see AAY36754-Y37949) which can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, perihepatitis, bartholinitis; pneumopathy in breast feeding infants; and venereal lymphogramulomatosis. The polypeptides of the invention may be of use in treating these diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  primers AAZ01426-206209 were used to amplify open reading frames
                                                                                                                                                                              eye disease; conventional trachoma; nonendemic trachoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
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                                                                                                                                                primer used to amplify an ORF of Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCR primer used to amplify an ORF of Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 10; DB 20;
Pred. No. 1.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20 BP; 0 A; 7 C; 3 G; 10 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome sequence of Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 1653; 1755pp; English.
                                                     AAZ04007 standard; DNA; 20 BP.
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                                                                                                                                                                                                                                                                                                                                                                                               98US-0107077.
97FR-0015041.
97FR-0016034.
                                                                                                                                                                                                                                                                                                                                                                    98WO-IB01939
                                                                                                                 07-OCT-1999 (first entry)
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Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10
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                                                                                                                                                                                                                                                                       Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-371125/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTTCTCTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           GEST ) GENSET
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28-NOV-1997;
17-DEC-1997;
                                                                                                                                                                                                                                                                                                      WO9928475-A2
                                                                                                                                                                                                                                                                                                                                                                  27-NOV-1998;
                                                                                                                                                                                                                                                                                                                                     10-JUN-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Griffais R;
                                                                                                                                                                                                                                                         Synthetic
                                                                                    AAZ04007:
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                     RESULT 34
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                                                                                                                                                PCR
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                                      AAZ04007
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                                                                                                                                                                                                                                                        The invention comprises the amino acid and coding sequence of the human interferon alpha 2 protein. The invention further relates to the dentification of single nucleotide polymorphisms (SNPs) within the human interferon alpha 2 gene. The DNA and protein sequences of the invention are useful for the treatment of: cancer; tumours; cardiovascular diseases; metabolic diseases; infectious diseases; central nervous system diseases; immunological diseases; wound healing; chemcherapy side effects; anaemia; osteoporosis; gastrointestinal diseases; veneral diseases; obesity; hepatitis; HIV/AIDS; infectious pneumonias; schizophrenia; depression; graft versus host disease; allergies; asthma; sociaesis; rheumatoid arthritis; Crohn's disease; ulcerative colitis; and genital warts. The present DNA sequence represents a primer that was used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCR primer used to amplify Mycoplasma hyopneumoniae P102 protein DNA
                                                                                                                                                                                      An isolated polynucleotide encoding interferon alpha 2 containing single nucleotide polymorphisms is useful in treating disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P102 protein; vaccine; antigen; diagnosis; swine; immunisation; enzootic pneumonia; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 10; DB 25; Length 20; Best Local Similarity 100.0%; Pred. No. 1.8e+04; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      to sequence the human interferon alpha 2 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 14 A; 1 C; 5 G; 0 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IOWA ) UNIV IOWA STATE RES FOUND INC.
                                                                                                                                                                                                                                 Example 4; Page 21; 42pp; English.
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                                                                      01-MAR-2001; 2001FR-0002843.
                                           01-MAR-2002; 2002EP-0290515
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                                                                                                                                                           WPI; 2003-185789/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hsu T, Minion FC;
                                                                                                  (GENO-) GENODYSSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-NOV-1998;
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               04-SEP-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                 Escary J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX60140/
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region and is used in the method of the invention. The method is for monitoring an immune response that involves somatic homologous recombination between elements of at least two segments associated with a hypervariable region, and comprises: (a) providing a polynucleotide sample from B- or T-cells, and amplifying it with: (i) a primer specific for a variable gene segment; and (ii) a primer specific for a constant or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a primer for the T cell receptor (TCR) variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCR primer; T-cell receptor; TCR; V region; immune response; arthritis; somatic homologous recombination; hypervariable region; spectratype determination; autoimmune response; multiple sclerosis; myasthenia gravis; muscular dystrophy; graft-infiltrating lymphocyte; tumour-infiltrating lymphocyte; ss.
                                                                                      PCR primers AAX60140-41 were used to amplify DNA encoding a Mycoplasma hyopneumoniae P102 protein clone. The P102 protein and its fragments are used in vaccines to protect against enzootic pneumonia, particularly in swine. Recombinant P102 polypeptides may be used as antigens for diagnostic purposes to determine whether or not a biological test sample contains M. hyponeumoniae antigens or antibodies. The P102 polypeptides or DNA sequences may also be used for immunising or protecting non-human animals, preferably swine, against M. hyponeumoniae infections, particularly enzootic pneumonia.
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Monitoring immune responses by analysing amplified B or T-cell nucleic acid - using primers specific for variable and constant or junction region gene segments, with separation of products by length, especially to monitor auto.immunity
                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                      y Match 100.0%; Score 10; DB 20; Length 21; Local Similarity 100.0%; Pred. No. 1.8e+04; hes 10; Conservative 0; Mismatches 0: Indela
Recombinant antigenic Mycoplasma hyponeumoniae protein
                                                                                                                                                                                                                                                                                                                  Sequence 21 BP; 12 A; 0 C; 7 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer Vbetal4 for T cell receptor V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 22; Column 38; 26pp; English.
                                             Example 2; Page 23; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CENT RES FOUND INC.
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92US-0868569.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CTICICITIT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 CTTCTCTTT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-APR-1994;
15-APR-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gorski J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV08126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia.
                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                   used to monitor autoimmune responses (including manners); j.e. to identify the predominant TCR in sites of autoimmune activity (e.g. in athritis, multiple sclerosis, mysthenia gravis and muscular dystrophy) or present in graft-infiltrating (in cases of organ rejection) or tumour-infiltrating lymphocytes. As each gene rearrangement is unique, each complementarity determining region 3 is a specific molecular fingerprint of the lymphocyte that generates it, and immune responses can be correlated with an increase in a particular TCR or immunoglobulin. Specific determination of two V beta families may be done simultaneously.
joining gene segment to produce amplification products (AP) that can be resolved at a difference in size of 2 or 3 bp, (c) separating the AP according to length; (d) detecting the range of lengths in the separated products to produce a 'spectratype' of the subject's immune response; and (e) comparing the spectratype with a predetermined standard to determine immune status or to monitor immune response. The method is specifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method of detecting Kawasaki disease by detecting an increase in Vbeta6.5 Voeta6.5/Vbeta2.1 positive T-cells. The sequences AAA9531-A95626 represent primers and probes used to PCR amplify and detect the level of expression of Valpha and Vbeta genes in T-cells in Kawasaki disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detection, diagnostic, Kawasaki disease, T-cell, PCR primer, probe,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 10; DB 20; Length 21; 100.0%; Pred. No. 1.8e+04; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 21 BP; 8 A; 3 C; 7 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 21 BP; 8 A; 3 C; 7 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCR Vbeta 14 subfamily probe VB14-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA95613 standard; DNA; 21 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SHIO ) SHIONOGI & CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CTTCTCTTT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 CTTCTCTTTT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene expression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-477722/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JP2000157297-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA95613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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This invention relates to the use of a novel enzyme in the production of an oil-producing organism. The enzyme catalyses the transfer of a fatty read for acyl-Coh to diacylglycerol to produce triacylglycerol of resulting in an increased oil content. Sequences AAH37155 and AAB97263 represent the Saccharomyces cerevisiae ARE1 coding and protein sequence respectively. ARE1 is used in the transformation or the organism of the invention. The invention is used to increase the oil content of oil crops such as rape, sunflower and oil palm, and other crops such as soy, maize, oat, potato, sugar beet and turnips. The invention could also be used to produce triacylglycerols in microorganisms. The present sequence represents a PCR primer used to amplify the Saccharomyces cerevisiae PDAT gene. The primer and PCR product are used in an example illustrating that triacylglycerol accumulation is reduced in yeast cells that lack the AREI cone. The primer is specifically used in the production of mutant yeast
                                                                                                                                                                                                                                                             Yeast, ARE 1, YCR048w; transgenic plant; oil production; acyl-CoA; fatty acid production; triacylglycerol; oil crop; rape; sunflower; PDAT; oil palm; soy; maize; oat; potato; sugar beet; turnip; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sandager L, Stahl U, Dahlqvist A, Lenman M, Ronne H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transforming oil-producing organisms with a gene encoding an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acyl-CoA:diacylglycerol acyltransferase, useful to generate agricultural crops with higher triacylglycerol content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                           Downstream PCR primer for amplification of PDAT gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 10; DB 22; 100.0%; Pred. No. 1.8e+04; ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SCAN-) SCANBI SCANDINAVIAN BIOTECHNOLOGY RES AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21 BP; 13 A; 3 C; 5 G; 0 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 6; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAS95067 standard; DNA; 21 BP.
                                                                                                                AAH27157 standard; DNA; 21 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-NOV-2000; 2000WO-SE02216.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0164859.
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                                                                                                                                                                                      08-AUG-2001 (first entry)
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es 10; Conservative
                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae.
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                     18 CTICICITI 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-329086/34.
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WO200134814-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stymne S;
                                                                                                                                                    AAH27157;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Banas A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           strains.
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                                                                             RESULT 40
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                                                                                               AAH27157,
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Gaps

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Query Match 100.0%; Score 10; DB 21; Length 21; Best Local Similarity 100.0%; Pred. No. 1.8e+04; Matches 10; Conservative 0; Mismatches 0; Indels

1 CTTCTCTTT 10

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The present sequence represents a potential triple-helix forming region. It can be used to demonstrate the assay of the invention. The assay comprises adding a sample containing double-stranded DNA test sequences, e.g. containing the present sequence, to an aqueous medium containing at reporter DNA, attached to a solid support, and reporter DNA, where either a part of the anchor DNA or reporter DNA designed to form a triple-strand structure with part of the test sequence. Triplex formation results in displacement of the reporter DNA hich is detected as an indication of the presence of the DNA test sequence. The method is used to detect DNA sequences, particularly for identification of bacteria (DV) detecting games for ribosomal RNA) in clinical samples, but also detection of oncogenes and Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human hydroxybutyryl coenzyme A dehydratase protein and its coding
                                                                                                                                                                                             Assay of genetic sequences based on triplex formation from double stranded analyte - and hybrid of anchor and reporter sequences, with reporter released if triplex formation occurs, used e.g. to identify bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human 3-hydroxyacyl-CoA-dehydratase cDNA specific PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; 3-hydroxyacyl-CoA-dehydratase; HCDase; hypothalamus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 10; DB 20; 100.0%; Pred. No. 1.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NANF-) NANFANG RES CENT STATE HUMAN GENE GROUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 22 BP; 1 A; 5 C; 0 G; 16 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                         Disclosure, Columns 15-16, 168pp, English.
                                                                                            (PROF-) PROFILE DIAGNOSTIC SCI INC.
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           93US-0173489.
                                            93US-0173489.
92US-0968436.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC66394 standard; DNA; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
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                                                                                                                                 Wang C;
                                                                                                                                                                   WPI; 1999-130384/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTICICITIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qian B,
         22-DEC-1993;
                                            22-DEC-1993;
                                                               29-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                 Hepburn AG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC66394/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a purified polymucleotide (I) encoding a protein sequence (II) encoded by a novel human gene, otoferlin (OTOF) or the long human otoferlin isoform in brain. (I) was identified as underlying an autosomal nonsyndromic prelingual deafness DFNB9, and is thus useful for detecting deafness disease in humans and for characterising the functions of proteins and genes encoding them in auditory function. AAS95022-AAS95248 represent human and mouse otoferlin coding sequences, PCR primers and related sequences of the
                                                                                                     Human; mouse; otoferlin; OTOF; brain; auditory function; PCR primer; autosomal nonsyndromic prelingual deafness; DFNB9; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human gene Otoferlin, underlying an autosomal recessive nonsyndromic prelingual deafness, DFNB9, and proteins encoded by the gene, implicated in deafness
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                                                                                                                                                                                                                                                                                                                                                                                                   Petit C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Triple helix forming nucleotides 9-30 of gamma-crystallin gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                             Cohen-Salmon M, El Amraoui A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21 BP; 10 A; 1 C; 8 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                  Human otoferlin exon PCR primer #32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 25; Page 17; 99pp; English
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                                                                                                                                                                                                                                                                                                                                         PASTEUR.
CENT NAT RECH SCI
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                                                                                                                                                                                                                                                                                                    24-MAR-2000; 2000US-191738P.
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                                   (first entry)
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Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX14678 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                             Grati M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTCTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-611499/70
                                                                                                                                                                                         WO200170972-A2
                                                                                                                                                                                                                                                                                                                                        (INSP ) INST
(CNRS ) CNRS
                                                                                                                                                           Homo sapiens
                               13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                             Yasunaga S,
Weil D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-MAR-1999
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Query Match

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                                                       (HCDase). The protein is expressed in normal hypothalamic tissue in humans. The invention includes human HCDase nuclectide and amino acid sequences, a method for the preparation of the protein and a method for detecting human HCDase nucleic acid and protein sequences in a sample. The present sequence represents a PCR primer specific for human HCDase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to an immunostimulatory composition, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA/RNA hybrid; phosphorothicate backbone; immunostimulatory; vaccine; infection; allergy; cancer; hypersensitivity; bio-warfare; immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV; immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy; antiinflammatory; antibacterial; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "optionally thymidine is replaced by uracil to form RNA or DNA/RNA hybrids. Thymidine is linked to at least one other base through a ribose sugar"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oligonucleotides, useful for enhancing an immune response or inducing cytokines, particularly for treating diseases, e.g. cancer, allergy or
                                                                                                                                                                                                                              Gaps
                                        This invention relates to a new human 3-hydroxyacyl-CoA-dehydratase
                                                                                                                                                                                                                               0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New immunostimulatory compositions comprising RNA/DNA hybrid
                                                                                                                                                                                                   Length 22;
                                                                                                                                                                                                                              Indels
                                                                                                                                                                                              100.0%; Score 10; DB 21; 100.0%; Pred. No. 1.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunostimulatory oligonucleotide SEQ ID NO: 612.
                                                                                                                                                                  Sequence 22 BP; 10 A; 2 C; 8 G; 2 T; 0 other;
                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 11; Page 63; 68pp; English.
              Example 1; Page 11; 21pp; Chinese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klinman DM;
                                                                                                                                                                                                                                                                                                                                                               ABL35686 standard; DNA; 22 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-2001; 2001WO-US18276.
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                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                         10; Conservative
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/*tag=
                                                                                                                                                                                                                                                       1 CTTCTCTTT 10
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                                                                                                                                                                                                                                                                                   CTTCTCTTT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-130570/17.
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                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIV infection
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                                                                                                                                                                                                                                                                                      16
                                                                                                                                                                                                                                                                                                                                                                                              ABL35686;
                                                                                                                                                                                              Query Match
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tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or colon, or carcinomas and sarcomas), autoimmune diseases or allergies (e.g. allergic filinitis, hay fever or food allergies), Lyme disease, hepatitis, HIV or malaria. The composition is also useful for treating, preventing or ameliorating the symptoms resulting from exposure to bio-warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is an immunostimulatory oligonucleotide described in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to an immunostimulatory composition, which comprises at least one oligonucleotide comprising both an RNA region and a DNA region. The composition is useful for enhancing an immune response or inducing cytokines. It can be used as a vaccine adjuvant and in treating diseases, including pathogenic infection, (non-)malignant tumours (e.g. cancers of the brain, lung, ovary, breast, prostate colon, or carcinomas and sarcomas), autoimmune diseases or allergies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine; infection; allergy; cancer; hypersensitivity; bio-warfare; immunostimulant; antiallergic; cytostatic; antimutcrobial; anti-HIV; immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy; antiinflammatory; antibacterial; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/note= "optionally thymidine is replaced by uracil to
form RNA or DNA/RNA hybrids. Thymidine is linked to at
least one other base through a ribose sugar"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New immunostimulatory compositions comprising RNA/DNA hybrid oligomucleotides, useful for enhancing an immune response or inducing cytokines, particularly for treating diseases, e.g. cancer, allergy or HIV infection
                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                       Length 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunostimulatory oligonucleotide SEQ ID NO: 613.
                                                                                                                                                                                                                 100.0%; Score 10; DB 24;
100.0%; Pred. No. 1.8e+04;
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                                                                                                                                                                         Sequence 22 BP; 1 A; 4 C; 3 G; 14 T; 0 other;
                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
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                                                                                                                                                                                           Query Match
Best Local Similarity 100.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                     of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABL35687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc RNA
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(e.g. allergic rhinitis, hay fever or food allergies), Lyme disease, hepatitis, HIV or malaria. The composition is also useful for treating, preventing or ameliorating the symptoms resulting from exposure to a bio-warfare agent, e.g. Ebola, Authrax or Listeria. The present sequence is an immunostimulatory oligonucleotide described in the exemplification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA/RNA hybrid, phosphorothioate backbone, immunostimulatory, vaccine; infection, allergy, cancer, hypersensitivity, bio-warfare, immunostimulant, antiallergic, cytostatic, antimicrobial, anti-HIV, immunosuppressive, protozoacide, virucide, hepatotropic, gene therapy, antiinflammatory, antibacterial; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "optionally thymidine is replaced by uracil to
form RNA or DNA/RNA hybrids. Thymidine is linked to at
least one other base through a ribose sugar"
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                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 10; DB 24; Length 22; 100.0%; Pred. No. 1.8e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunostimulatory oligonucleotide SEQ ID NO: 614.
                                                                                                                                                                                                                                                                        Sequence 22 BP; 1 A; 4 C; 4 G; 13 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Klinman DM;
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                                                                                                                                                                                                                                                                                                                                                 Query Match 100.

Best Local Similarity 100.

Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CTTCTCTTTT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 CTTCTCTTTT 16
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                                                                                                                                                                                                       of the invention.
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AAX09121-X10268 are allele-specific oligonucleotide primers used in the isolation of various biallelic polymorphic markers found in the human genome (represented in AAX10269-X1293). These primers can be used in a method for determining polymorphic forms in an individual for use in e.g. forensics, paternity testing or for phenotypic typing for diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary apheroxytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Bhlers-Danlos syndrome, osteogenesis imperfecta, acute intermittent porphyria, autoimmune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such as longevity, appearance (e.g. baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid eggments can also be used to produce medicaments for the treatment or prophylaxis of such diseases.
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                   bio-warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is an immunostimulatory oligonucleotide described in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament; treatment; marker; primer; ss.
                                                                                                                                                                                  Gaps
  preventing or ameliorating the symptoms resulting from exposure to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid segments from the human genome - used for determining polymorphic forms for use in e.g. forensics, paternity
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                                                                                                                                        100.0%; Score 10; DB 24; Length 22; 100.0%; Pred. No. 1.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human biallelic polymorphic marker downstream primer #328.
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                                                                                               Sequence 22 BP; 1 A; 4 C; 2 G; 15 T; 0 other;
                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang D;
                                                                                                                                                                                                                                                                                                                                                              AAX10022 standard; DNA; 23 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             24-MAR-1999 (first entry)
                                                                                                                                                         Local Similarity 100.
nes 10; Conservative
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                                                             of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                       AAX10022;
                                                                                                                                        Query Match
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The primers AAT10352-97 were used to PCR amplify the T cell receptor beta chain variable regions from T cell culture clones, isolated from the synovial joint fluid of 11 patients suffering from thematoid arthritis. The coding sequences were shown to contain the nucleotide sequence AAT07409. The encoded polypeptide can be used as an immunogenic cpd. for the detection of or predisposition to an immune disease, or for use as a waccine for prevention or treatment of an immune disease. principle can emplifies the variable region from the 14.1 family of clones.
                                                                                                       T cell receptor, beta chain, variable region, rheumatoid arthritis, synovial joint fluid, PCR, amplification, primer, immunogen, vaccine,
                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide contained in the variable region of a T-cell receptor beta chain - specifically associated with immune disease, esp. rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibody; T-cell receptor; beta chain; human immunodeficiency virus; HIV; blood; attenuation; primer; PCR; amplification; variable region; constant region; TCR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primer V-beta(14) for T-cell receptor beta chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 10; DB 16; Length 24; 100.0%; Pred. No. 1.8e+04; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                               Van Der Maaden JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Page 24; 55pp; English.
                                                                          T-cell receptor primer Vbetal4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1116/c
AAT98116 standard; DNA; 24 BP.
                                                                                                                                                                                                                                                                                                             94EP-0200454.
                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                             Rijnders AWM,
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                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-311502/40.
                                                                                                                                            immune disease; ss.
                                         02-APR-1996
                                                                                                                                                                                                                                                                                                             23-FEB-1994;
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                                                                                                                                                                                                                                           31-AUG-1995.
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                                                                                                                                                                                                                                                                                                                                                                             Graus JPM,
                                                                                                                                                                             Synthetic.
          AAT10390;
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                                      Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nishioka K, Sakoda H, Yamamoto K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 24;
                                                                                                                                                                                                                                                                                                                                                                 RT-PCR; polymerase chain reaction; amplification; SSCP; single-strand conformation polymorphism; variable domain; subtype beta 14; ss.
                                                                     Indels
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                                    Score 10; DB 19;
Pred. No. 1.8e+04;
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100.0%; Pred. No. 1.8e+04;
tive 0; Mismatches 0;
Sequence 23 BP; 16 A; 0 C; 7 G; 0 U; 0 other;
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                                                                                                                                                                                                                                                                                                                                  T-cell antigen receptor V-beta14 PCR primer.
                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Page 13; 47pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT10390 standard; cDNA; 24 BP.
                                    100.0%;
100.0%;
                                                                                                                                                                                                                     AAQ50920 standard; DNA; 24 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93WO-JP00577.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92JP-0111467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (LTTL-) LTT INST CO LTD.
(TAIS ) TAISHO PHARM CO LTD.
                                                                                                                                                                                                                                                                                                      (first entry)
                             Query Match
Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mizushima Y,
                                                                                                  1 CTICICITIT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10
                                                                                                                     CTTCTCTTTT 4
                                                                                                                                                                                                                                                                                      (updated)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9322455-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-APR-1992;
                                                                                                                                                                                                                                                                                     25-MAR-2003
19-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic,
                                                                                                                                                                                                                                                     AAQ50920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ikeda Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT10390/c
ID AAT103
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Matches
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AAQ50920/c
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This invention describes novel method for binding free antibodies having a paratope specific to an epitope on a T cell receptor (TCR-V beta) while providing an immunogenic substance able to raise anti-idiotypic antibodies bound at the same paratope specific to the epitope on the TCR-V beta and introducing this into a person to raise anti-idiotypic antibodies. The products of the invention antibody binding affinities are useful in assays which detect the presence of CD4+ cell subpopulations carrying particular V beta components of the TCR-V beta in people infected with acquired immune deficiency syndrome (AIDS). AAXBB119-X88169 represents primers used in
                                                                       which have a paratope capable of binding to an epitope of a T cell subject variable beta (TCR-V beta) region. The method comprises administering a binding agent homologous with the TCR-V beta epitope. The binding agent is useful in assays for detecting various (The binding agent is useful in assays for detecting various The binding agent is also useful in the treatment of people infected with HIV where it is able to remove an antibody able to bind with an epitope on a TCR-V beta cell in the blood of an infected person. PCR primers AAX85943-71 represent T cell receptor beta-chain primers used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T cell receptor; beta chain; primer; antibody; paratope; AIDS; vaccine; epitope; TCR-V beta; immunogenic; anti-idiotypic; antiviral; detection; CD4+ cell subpopulation; acquired immune deficiency syndrome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diagnosis and treatment of acquired immune deficiency syndrome onset
                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 10; DB 20; Length 24; 100.0%; Pred. No. 1.8e+04;
                                                           specification describes a method for the diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                 Sequence 24 BP; 10 A; 3 C; 7 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T cell receptor beta chain primer V-betal4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Column 11-12; 42pp; English.
              Example 1; Column 11; 42pp; English.
                                                                                                                                                                                                                                                                                                                  in the course of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX88135 standard; DNA; 24 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94US-0408011.
95US-0488209.
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                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CTICICITIT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-OCT-1994;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-NOV-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX88135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primi D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX88135,
            %X000000000000X8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method for removing an antibody specific for TCR-V beta (T-cell receptor V beta protein) from an HIV-infected person by removing blood from the preson, removing the antibody from the blood and reintroducing the blood into the person, thus allowing attenuation or aversion of immunodeficiency. The primers AAT98100-T98150 are used to check the efficiency of removal by detecting expression of the TCR-V-beta and V-alpha genes in a blood sample after treatment. This primer is targetted to the variable region sequence and can be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Acquired immune deficiency syndrome; free antibody; paratope; epitope; T cell receptor variable beta region; TCR-V beta region; binding agent; CD4+ T cell; HIV; PCR primer; ss.
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                                                                                                                                                                                                                                                                               Removal of T-cell receptor-specific antibody from blood of HIV-infected person - by extracorporeal blood treatment, to attenuate or avert development of AIDs from HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR primer used to amplify T cell receptor beta-chain cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 10; DB 18; 100.0%; Pred. No. 1.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 24 BP; 10 A; 3 C; 7 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the amplification with primer AAT98100.
                                                                                                                                                                                                                                                                                                                                                                                Example 1; Column 11; 43pp; English
                                                                                                                                       (CONS-) CONSORZIO BIOTECNOLOGIE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CONS-) CONSORZIO BIOTECNOLOGIE,
                                            92US-0973485.
94US-0408011.
95US-0488212.
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  95US-0488212
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94US-0408011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX85959 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                        WPI; 1997-456759/42.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
  07-JUN-1995;
                                              09-NOV-1992;
                                                                          18-OCT-1994;
                                                                                             07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-OCT-1994;
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                                                                                                                                                                                         Primi D;
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AAX85959/
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                                                                                                                                                                                                                                             Wang Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence listing.
                                                                                                                                 WO200127332-A1.
                                                                                                                                                                                                 13-OCT-1999;
                                                                                                                                                      19-APR-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human dihydroorotase 11 for diagnosing and treating malignant tumour, haemopathy, human immunodeficiency virus infection, immunological diseases and various inflammations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    virucidal, immunomodulatory, antiinflammatory and haemostatic activity. The protein and encoding polynucleotide are used in diagnosis and treatment of malignant tumour, haemopathy, human immunodeficiency virus (HIV) infection, immunological diseases and various inflammations. The polynucleotide is useful in gene therapy. The present sequence is that of a PCR primer, useful to the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                 Gaps
                                                                                                                                                                                                                                                      Human, dihydroorotase 11; cytostatic; virucidal; immunomodulatory; antiinflammatory; haemostatic; malignant tumour; HIV; infection; human immunodeficiency virus; immunological disease; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to human dihydroorotase 11 with cytostatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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0
                                          'Match 100.0%; Score 10; DB 20; Length 24; Local Similarity 100.0%; Pred. No. 1.8e+04; les 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 10; DB 22; Length 24; 100.0%; Pred. No. 1.8e+04;
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0
                                                                                                                                                                                                                                  Human dihydroorotase 11 PCR primer SEQ ID NO 4.
                      Sequence 24 BP; 10 A; 3 C; 7 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 24 BP; 8 A; 3 C; 8 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Preq. No.
                                                                                                                                                                                                                                                                                                                                                                                                                           (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Page 17; 34pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH19640 standard; DNA; 24 BP.
                                                                                                                                                                  AAI99892 standard; DNA; 24 BP.
the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                               26-MAR-2001; 2001WO-CN00421
                                                                                                                                                                                                                                                                                                                                                                                                    27-MAR-2000; 2000CN-0115157.
                                                                                                                                                                                                             30-JAN-2002 (first entry)
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Les 10; Conservative
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                                                                                                             18 CTTCTCTTT
                                                                                                                                                                                                                                                                                          PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                    WO200173054-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mao Y, Xie Y;
                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                          04-OCT-2001.
                                                                                                                                                                                        AAI99892;
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                                          Query Match
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                                                                Matches
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                                                                                                                                              RESULT 53
                                                                                                                                                       AA199892,
SXCC
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T cell receptor; TCR; receptor; variable beta peptide; BV peptide; TCRV; T cell variable gene; T cell regulatory activity; autoimmune disease;
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                                                                                                                                                  Melon, cucurbit, Fusarium wilt, infection, resistance, susceptibility, genotype identification, polymerase chain reaction, PCR; Fusarium oxysporum; marker, PCR primer, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying cucurbit genotypes to determine susceptibility or resistance to Fusarium wilt disease, comprises using the polymerase chain reaction (PCR) and comparing the PCR product with known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T cell receptor (TCR) variable beta (BV) peptide RT-PCR primer #16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The present sequence is given as SEQ ID NO: 3 in Figure 2, but it is different to the sequence given as SEQ ID NO: 3 in the
                                                                           Melon fusarium wilt-resistance marker FM forward primer FM-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 10; DB 22; Length 24; 100.0%; Pred. No. 1.8e+04; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 24 BP; 14 A; 1 C; 8 G; 1 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   resistant/susceptible genotypes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 10; Fig 2; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABS71673 standard; DNA; 24 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-OCT-2000; 2000WO-US28633.
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01-AUG-2001 (first entry)
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                                                                                                                                                                                                                                                                                                              The invention relates to a method for identifying a T cell receptor variable (TCRN) gene expressed by target T cells in an individual, comprising determining expression of TCRV genes by activated T cells from the individual and determining regulatory activity elicited in response to TCRV peptides from the individual. A preferentially expressed TCRV spetides from the individual, A preferentially expressed TCRV identified as a variable gene expressed by target T cells. The method is used to identify disease-associated T cells in an individual so that individualised theraptes can be designed to prevent or treat the disease, particularly an autoimmune disease, especially multiple sclerosis. This sequence represents a reverse transcriptase PCR (RT-PCR) primer used in analysis of expression of DNA encoding TCR variable beta (BV) peptides.
                                                                                                                                                                                                                          Identifying a T cell receptor variable gene expressed by target T cells in an individual is useful to identify disease-associated T cells for design of individualised therapies, particularly for autoimmune disease
multiple sclerosis; human; reverse transcriptase; RT-PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibacterial; antiprotozoal; antifungal; cell growth inhibitor;
protozoa; bacterium; fungus; amoeba; mycoplasma; murA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 10; DB 24; Length 24; 100.0%; Pred. No. 1.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 24 BP; 10 A; 3 C; 7 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B. subtilis knock-out PCR primer KO murA R1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                        Example 2; Page 11; 20pp; English
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                                                                                                  10-MAY-2001; 2001US-0853830
                                                                                                                           12-MAY-2000; 2000US-203984P
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Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                  (VAND/) VANDENBARK A A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CTICTCTITI 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fola; yibD; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus subtilis
                                               US2002107388-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200216940-A2
                                                                                                                                                                            Vandenbark AA;
                       Homo sapiens
                                                                          08-AUG-2002
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The invention relates to a method of identifying a molecular target of a cell growth inhibiting compound by: (a) identifying a compound or cell growth inhibiting growth in a population of cells; (b) performing target prediction processes to identify a modulated gene or gene product; or product identified by other prediction processes. The method is used for identifying the molecular target of a cell growth inhibitor. The cells are selected from organisms such as protozoa, bacterium, fungus, amoeba are selected from organisms such as protozoa, bacterium, fungus, amoeba arget-based screening. The method relies first on identification of compounds with good whole cell activity and then provides methods to in isolation, but in combination of at least two (preferably at least three) provides a higher success in identifying the molecular target.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; BolA structural domain zinc finger protein 37; malignant tumour; nosohaemia; HIV infection; immunological disease; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polypeptide-human Bola structural domain zinc finger protein 37 and polynucleotide for said polypeptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human BolA structural domain zinc finger protein 37 PCR primer 1.
                                                                                                                         Identification of a molecular target of a cell growth inhibitor, comprises target prediction processes to identify at least one modulated gene or gene product
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                                         Bunker C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 24 BP; 9 A; 4 C; 6 G; 5 T; 0 other;
                                       Moir DT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          demonstrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BODA-) BODAO GENE TECH CO LTD SHANGHAI
                                                                                                                                                                                                               Example 2; Page 97; 157pp; English.
                                         Opperman T,
(GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABA04339 standard; DNA; 24 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JAN-2000; 2000CN-0111611.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-JAN-2000; 2000CN-0111611
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Best Local Similarity 100.
Matches 10; Conservative
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                                       Ling LL,
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                                                                                 WPI; 2002-329705/36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xie Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CN1307053-A.
                                       Sulavik M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16
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                                      The present invention describes human BolA structural domain zinc finger protein 37 (1). (1) can be used in the treatment of various diseases, such as malignant tumour, nosohaemia, HU infection, immunological diseases and inflammations. The present sequence represents a PCR primer for human BolA structural domain zinc finger protein 37, which is used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a method of arraying genome clones. The method comprises: (a) clones of the genomic libraries contained in multiwell plates numbered for discrimination are mixed in each of the multiwell plates; (b) a primer designed based on the chromosome marker sequence is added to the mixture to carry out an amplification reaction; (c) a signal corresponding to the marker is detected from the resultant amplified product to specify the discrimination Nos. of the multiwell plates containing the clones having said marker sequence; (d) the corder of the markers is changed so that the same discrimination Nos. succeed to the marker multiple containing the clones having said marker sequence; (d) the corder of the marker is changed so that the same discrimination Nos. succeed the maximum in the specified discrimination Nos. to array the multiwell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plates; (e) the clones in the multiwell plates of the specified discrimination Nos. are mixed respectively in each wells of longitudinal and lateral directions; (f) the mixed clones are cultured and the
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis;
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                                                                                                                                                                                                                                           100.0%; Score 10; DB 24; Length 24; 100.0%; Pred. No. 1.8e+04;
                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human chromosome 21q22.1 PCR primer SEQ ID NO:2633.
Example 3; Page 17 (Disclosure); 35pp; Chinese.
                                                                                                                                                                                                  Sequence 24 BP; 12 A; 4 C; 4 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                         in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 6; Page 57; 528pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL45589 standard; DNA; 24 BP.
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                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.(
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                               1 CTTCTCTTT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genome; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JP2001321190-A.
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  8 X C C C C C C X X
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In a specific example of a novel process for amplifying an amount (known or unknown) of a double-stranded nucleic acid segment to produce single-stranded nucleic acid, the Staphylococus aureus carating amount of the nucleic acid, the Staphylococus aureus exfoliative toxin A (ETA) gene was used as the DNA template. The region comprising nucleotides 165-436 was amplified by symmetric, asymmetric or competitor primer asymmetric PCR using the primers of TA-A2 and ETA-B (see AAT76779). For asymmetric PCR, the amount of primer ETA-B was reduced and for competitor primer and AAT76779). For asymmetric PCR, the asymmetric PCR a competitor primer ETA-B2 (see AAT76780) was added with upstream primer ETA-A2 after the initial cycling reaction. PCR products containing ETA-Specific sequences were detected adioactively by a capture system which employed a bifunctional capture probe ETA-CP (see AAT76781 and AAT76782). ETA-CP was designed to capture the amplified sense strand onto capture membranes through hybridisation between the first 40 nucleotides of ETA-CP (and nucleotides 31-360 of the ETA gene and through hybridisation of the ETA-CP (and through hybridisation between the first 40 nucleotides of ETA-CP (and nucleotides 389-410 of the ETA gene was used to detect the amplicons. Results showed that hybridisation of the capture probe and label probe to the denatured symmetric PCR product was much less efficient than hybridisation to the single-stranded PCR products of the asymmetric and competitor
                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus exfoliative toxin A competitor primer ETA-B2.
                                                                                                                                                                                                                                                                                                                                                                                       Asymmetric polymerase chain reaction; nucleic acid amplification; PCR; detection; assay; exfoliative toxin A; ETA; skin lesion; competitive primer; capture probe; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quantitative nucleic acid amplification - by competitor primer
                                        Length 24;
                                                                           Indels
                                  100.0%; Score 10; DB 24; 100.0%; Pred. No. 1.8e+04;
Sequence 24 BP; 12 A; 2 C; 6 G; 4 T; 0 other;
                                              100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           asymmetric polymerase chain reaction
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                                                                                                                                                                                                                                        AAT76780 standard; DNA; 25
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                                                    Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                               19 CTTCTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US5627054-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-MAY-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                               AAT76780;
                                  Query Match
                                                                                                                                                                                                     RESULT 59
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Sequence 25 BP; 9 A; 2 C; 9 G; 5 T; 0 other;
       example from the invention.
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                                                                                                                                                                                                                                                                                                                                 RESULT 61
                                                                                                                                                                                                                                                                                                                                                        ABV82472,
                                                                                                                                                                                                                                                      셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to human testis expressed Patched like protein (HTPL, see ABV78759 to ABV79762 and ABB98519 to ABB98520). HTPL has two isoforms, with a few single base pair differences between the two. One of the single base pair changes introduces a premature stop codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL shares an overall structure organisation with the Patched protein. The shares an overall structures strongly imply that HTPL plays a role similar to that of Patched, and is a potential tumour suppressor. HTPL is important in regulating male germ cell development, and the HTPL gene was mapped to human chromosome 10pl2.1. HTPL and its coding sequence are useful for diagnosing a disorder caused by mutation in HTPL, and in the tapy and manufacture of a medicament for treatment or prevention of such disorder associated with decreased expression or activity of human HTPL. Such disorders include disorders of testis, or adreanal, adult and foetal liver, bone marrow, brain, kidney, lung, placenta, prostate. Skeletal muscle or colon function. HTPL proteins and nucleic acids are clinically useful diagnostic markers and potential therapeutic agents for male infertility and cancer. The present oligonucleotide was used in an
                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1; human testis expressed Patched like protein; testis; adrenal; liver; human cell development; bone marrow; brain; kidney; lung; placenta; prostate; skeletal muscle; colon; male infertility; cancer; ss.
                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated human testis expressed Patched like protein (HTPL), useful for identifying agonist and antagonist and specific binding partners, and for treating subjects having defects in HTPL -
                                                                                                      ;
                                                     Length 25;
                                                                                                    Indels
                                                   100.0%; Score 10; DB 18;
100.0%; Pred. No. 1.8e+04;
iive 0; Mismatches 0;
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Sequence 25 BP; 4 A; 5 C; 3 G; 8 T; 5 other;
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                                                                                                                                                                                                                                                                                                                              ABV82471 standard; DNA; 25 BP
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30-JAN-2001; 2001WO-US00665.
30-JAN-2001; 2001WO-US00667.
30-JAN-2001; 2001WO-US00669.
30-JAN-2001; 2001WO-US00669.
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09-OCT-2001; 2001US-0327898.
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                                           Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                       CTICICITIT 10
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The present invention relates to human testis expressed Patched like protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL has two isoforms, with a few single base pair differences between the two. One of the single base pair changes introduces a premature stop codon in HTPL-S (S for short) compared to HTPL-L(L for long). HTPL shares an overall structure organisation with the Patched protein. The shares an overall structure organisation with the Patched protein. The compared to than of Patched, and is a potential tumour suppressor. HTPL plays a role similar to that of Patched, and is a potential tumour suppressor. HTPL gene was important in regulating male germ cell development, and the HTPL gene was important in regulating male germ cell development, and the HTPL gene useful for diagnosing a disorder caused by mutation in HTPL, and in therapy and manufacture of a medicament for treatment or prevention of such disorder associated with decreased expression or activity of human HTPL. Such disorders include disorders of testis, or adrenal and the disorder colon function. HTPL proteins and nucleic acids are skeletal muscle or colon function. HTPL proteins and nucleic acids are
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           Length 25;
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       Score 10; DB 24;
Pred. No. 1.8e+04;
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tive 0;
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Query Match
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23-MAY-2001;
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The present invention relates to human testis expressed Patched like protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL two. One of the single base pair changes introduces a premature stop codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL shares an overall structure organisation with the Patched protein. The shared structural features strongly imply that HTPL plays a role similar to that of Patched, and is a potential tumour suppressor. HTPL is important in regulating male germ cell development, and the HTPL gene was mapped to human chromosome 10pl2.1. HTPL and its coding sequence are useful for diagnosing a disorder caused by mutation in HTPL, and in the therapy and manufacture of a medicament for treatment or prevention of such disorder associated with decreased expression or activity of human HTPL. Such disorders include disorders of testis, or adrenal, adult and
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clinically useful diagnostic markers and potenial therapeutic agents male infertility and cancer. The present oligonucleotide was used in example from the invention.
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100.0%; Pred. No. 1.8e+04;
ive 0; Mismatches 0; Indels
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                                                                        Sequence 25 BP; 8 A; 2 C; 9 G; 6 T; 0 other;
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foetal liver, bone marrow, brain, kidney, lung, placenta, prostate, skeletal muscle or colon function. HTPL proteins and nucleic acids are clinically useful diagnostic markers and potenial therapeutic agents for male infertility and cancer. The present oligonucleotide was used in an example from the invention.
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30-JAN-2001; 2001W0-US00667.
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human testis expressed Patched like protein; testis, adrenal; liver;
male germ cell development; bone marrow; brain; kidney; lung; placenta;
prostate; skeletal muscle; colon; male infertility; cancer; ss.
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30-JAN-2001; 2001WO-US00664.
30-JAN-2001; 2001WO-US00665.
30-JAN-2001; 2001WO-US00667.
30-JAN-2001; 2001WO-US00669.
30-JAN-2001; 2001WO-US00669.
23-MXY-2001; 2001US-US0669.
09-OCT-2001; 2001US-084761.
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important in regulating male germ cell development, and the HTPL gene was mapped to human chromosome 10p12.1. HTPL and its coding sequence are useful for diagnosing a disorder caused by mutation in HTPL, and in therapy and manufacture of a medicament for treatment or prevention of such disorder associated with decreased expression or activity of human HTPL. Such disorders include disorders of testis, or adremal, adult and foetal liver, bone marrow, brain, kidney, lung, placenta, prostate, skeletal muscle or colon function. HTPL proteins and nucleic acids are clinically useful diagnostic markers and potenial therapeutic agents for male infertility and cancer. The present oligonucleotide was used in an example from the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1; human testis expressed Patched like protein; testis; adrenal; liver; male germ cell development; bone marrow; brain; kidney; lung; placenta; prostate; skeletal muscle; colon; male infertility; cancer; ss.
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09-OCT-2001; 2001US-0327898
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Best Local Similarity 100.
Matches 10; Conservative
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ABV82477/c
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shared structural features strongly imply that HTPL plays a role similar to that of Patched, and is a potential tumour suppressor. HTPL is important in regulating male germ cell development, and the HTPL gene was mapped to human chromosome 10p12.1 HTPL and its coding sequence are useful for diagnosing a disorder caused by mutation in HTPL, and in therapy and manufacture of a medicament for treatment or prevention of such disorder associated with decreased expression or activity of human HTPL. Such disorders include disorders of testis, or adrenal, adult and foetal liver, bone marrow, brain, kidney, lung, placenta, prostate, skeletal muscle or colon function. HTPL proteins and nucleic acids are clinically useful diagnostic markers and potenial therapeutic agents for example from the invention.
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09-OCT-2001; 2001US-0327898.
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                                                           shares an overall structure organisation with the Parched protein. The shared structural features strongly imply that HTPL plays a role similar to that of Patched, and is a potential tumour suppressor. HTPL is important in regulating male germ cell development, and the HTPL gene was mapped to human chromosome 10pl2.1. HTPL and its coding sequence are useful for diagnosing a disorder caused by mutation in HTPL, and in therapy and manufacture of a medicament for treatment or prevention of such disorder associated with decreased expression or activity of human HTPL. Such disorders include disorders of testis, or adremal, adult and foetal liver, bone marrow, brain, kidney, lung, placenta, prosetate, stellar muscle, or colon function. HTPL proteins and nucleic acids are
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two. One of the single base pair changes introduces a premature stop codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL shares an overall structure organisation with the Patched protein. The shares an overall structure organisation with the Patched protein. The shared structural features strongly imply that HTPL plays a role similar to that of Patched, and is a potential tumour suppressor. HTPL gene was important in regulating mals germ cell development, and the HTPL gene was mapped to human chromosome 10p12.1. HTPL and its coding sequence are useful for diagnosing a disorder caused by mutation in HTPL, and in the harpy and manufacture of a medicament for treatment or prevention of such disorder associated with decreased expression or activity of human forth disorders include disorders of testis, or adrenal, adult and foetal liver, bone marrow, brain, kidney, lung, placenta, prostate, sheltel muscle or colon function. HTPL proteins and nucleic acids are clinically useful diagnostic markers and potenial therapeutic agents for male infertility and cancer. The present oligonucleotide was used in an example from the invention.
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2001WO-US00667.
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09-OCT-2001; 2001US-0327898.
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Best Local Similarity 100.
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30-JAN-2001;
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23-MAY-2001;
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Example 2; Page 552; 718pp; English.

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The present invention relates to human testis expressed Patched like protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL has two isoforms, with a few single base pair differences between the two oisoforms, with a few single base pair differences between the two of the single base pair changes introduces a premature stop codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL starts an overall structure organisation with the Patched protein. The shared structural features strongly imply that HTPL plays a role similar to that of Patched, and is a potential tumour suppressor. HTPL is important in regulating male germ cell development, and the HTPL gene was mapped to human chromosome loppi.1. HTPL and its coding sequence are useful for diagnosing a disorder caused by mutation in HTPL, and in therapy and manufacture of a medicament for treatment or prevention of therapy and manufacture of a medicament for treatment or prevention of therapy and manufacture of a medicament for treatment or prevention of therapy and soorder associated with decreased expression or activity of human HTPL. Such disorders include disorders of testis, or adrenal, and foetal liver, bone marrow, brain, kidney, lung, placenta, prostate, skeletal muscle or colon function. HTPL proteins and nucleic acids are clinically useful diagnostic markers and potenial therapeutic agents for male infertility and cancer. The present oligonucleotide was used in an example from the invention.
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2001WO-US00668
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Novel isolated human testis expressed Patched like protein (HTPL), useful for identifying agonist and antagonist and specific binding partners, and for treating subjects having defects in HTPL -

WPI; 2002-676582/73.

2001WO-US00669 2001US-0864761

30-JAN-2001;

23-MAY-2001;

-OCT-2001; 2001US-0327898

(AEOM-) AEOMICA INC

Zhan J;

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The present invention relates to human testis expressed Patched like protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL has two isoforms, with a few single base pair differences between the two. One of the single base pair changes introduces a premature stop codon in HTPL-S (S for short) compared to HTPL-L. (L for long). HTPL shares an overall structure organisation with the Patched protein. The shares an overall structure organisation with the Patched protein. The shares an overall structure organisation with the Patched protein. The shared structural features strongly imply that HTPL plays a role similar to that of Patched, and is a potential tumour suppressor. HTPL gene was important in regulating male germ cell development, and the HTPL gene was mapped to human chromosome 10p12.1. HTPL and its coding sequence are useful for diagnosing a disorder caused by mutation in HTPL, and in therapy and manufacture of a medicament for treatment or prevention of such disorders associated with decreased expression or activity of human HTPL. Such disorders include disorders of testis, or adrenal, adult and foetal liver, bone marrow, brain, kidney, lung, placenta, prosette, skeledal muscle or colon function. HTPL proteins and nucleic acids are clinically useful diagnostic markers and potenial therapeutic agents for male infertility and cancer. The present oligonucleotide was used in an example from the invention.
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iive 0; Mismatches 0;
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30-JAN-2001; 2001WO-US00665.
30-JAN-2001; 2001WO-US00667.
30-JAN-2001; 2001WO-US00669.
23-MAY-2001; 2001WO-US00669.
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The present invention relates to human testis expressed Patched like protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL has two isoforms, with a few single base pair differences between the two. One of the single base pair changes introduces a premature stop codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL shares an overall structure organisation with the Patched protein. The shares an overall structure organisation with the Patched protein. The contact of Patched, and is a potential tumour suppressor. HTPL is important in regulating male germ cell development, and the HTPL gene was important in regulating male germ cell development, and the HTPL gene was useful for diagnosing a disorder caused by mutation in HTPL, and in therapy and manufacture of a medicament for treatment or prevention of such disorder associated with decreased expression or activity of human HTPL. Such disorders include disorders of testis, or adrenal, adult and foctal liver, bone marrow, brain, kidney, lung, placenta, prostate, skeletal musch, discontaction. HTPL proteins and muleic acids are
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partners, and for treating subjects having defects in HTPL
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30-JAN-2001; 2001WO-US00669.
23-MAY-2001; 2001US-0864761.
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30-JAN-2001; 2
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The present invention relates to human testis expressed Patched like protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL has two isoforms, with a few single base pair differences between the two. One of the single base pair changes introduces a premature stop codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL shares an overall structure organisation with the Patched protein. The shares an overall structure organisation with the Patched protein. The shares an overall structure organisation with the Patched protein. The shares at organisation miply that HTPL plays a role similar to that of Patched, and is a potential tumour suppressor. HTPL is important in regulating male germ cell development, and the HTPL gene was important in regulating male germ cell development, and the HTPL gene was usupported to human chromosome 10pl2.1. HTPL and its coding sequence are useful for diagnosing a disorder suused by mutation in HTPL, and in therapy and manufacture of a medicament for treatment or prevention of therapy and manufacture of a medicament for treatment or prevention of therapy and manufacture of a medicament for treatment or prevention of foetal liver, bone marrow, brain, kidney, lung, placenta, prostate, skeletal muscle or colon function. HTPL proteins and nucleic acids are clinically useful diagnostic markers and potenial therapeutic agents for male infertility and cancer. The present oligonucleotide was used in an example from the invention.
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Novel isolated human testis expressed Patched like protein (HTPL), useful for identifying agonist and antagonist and specific binding partners, and for treating subjects having defects in HTPL -
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100.0%; Score 10; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels
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                                                                                   Example 2; Page 552; 718pp; English
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2001WO-US00668.
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2001US-0864761.
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The present invention relates to human testis expressed Patched like protein (HTPL, see ABV78759 to ABV8762 and ABB98519 to ABB98520). HTPL has two isoforms, with a few single base pair differences between the two. One of the single base pair changes introduces a premature stop codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL shares an overall structure organisation with the Patched protein. The shares an overall structure organisation with the Patched protein. The cothat of Patched, and is a potential tumour suppressor. HTPL gene was important in regulating male germ cell development, and the HTPL gene was mapped to human chromosome 10pl2.1. HTPL and its coding sequence are useful for diagnosing a disorder caused by mutation in HTPL, and in therapy and manufacture of a medicament for treatment or prevention of such disorder associated with decreased expression or activity of human fortal liver, bone marrow, brain, kidney, lung, placenta, prostate, skeletal muscle or colon function. HTPL proteins and nucleic acids are clinically useful diagnostic markers and potenial therapeutic agents for male infertility and cancer. The present oligonucleotide was used in an example from the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
human testis expressed Patched like protein; testis; adrenal; liver;
male germ cell development; bone marrow; brain; kidney; lung; placenta;
prostate; skeletal muscle; colon; male infertility; cancer; ss.
                                                                   Novel isolated human testis expressed Patched like protein (HTPL), useful for identifying agonist and antagonist and specific binding partners, and for treating subjects having defects in HTPL -
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                                                                                                                                         Example 2; Page 553; 718pp; English.
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2001US-0327898
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Best Local Similarity 100.
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30-JAN-2001; 2
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30-JAN-2001; 2
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23-MAY-2001;
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      Zhan J;
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                                                                                                                             The present invention relates to human testis expressed Patched like protein (HTPL, see ABV78759 to ABV7862 and AB98519 to AB98520). HTPL has two isoforms, with a few single base pair differences between the two. One of the single base pair changes introduces a premature stop codon in HTPL-S (S for short) compared to HTPL-L (I for long). HTPL shared structural features strongly imply that HTPL plays a role similar to that of Patched, and is a potential tumour suppressor. HTPL is important in regulating male germ cell development, and the HTPL gene was composed to human chromosome 10pl2.1 HTPL and its coding sequence are useful for diagnosing a disorder caused by mutation in HTPL, and in there is manufacture of a medicament for treatment or prevention of such disorders include disorders of testis, or adrenal, adult and coteral liver, bone marrow, brain, kidhey, lung, placenta, prostate, continically useful diagnostic markers and potental therapeutic agents for example from the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
human testis expressed Patched like protein; testis; adrenal; liver;
male germ cell development; bone marrow; brain; kidney; lung; placenta;
prostate; skeletal muscle; colon; male infertility; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                             Novel isolated human testis expressed Patched like protein (HTPL), useful for identifying agonist and antagonist and specific binding partners, and for treating subjects having defects in HTPL -
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100.0%; Pred. No. 1.8e+04;
ive 0; Mismatches 0;
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2001WO-US00667.
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Best Local Similarity 100...
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WPI; 2002-676582/73.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clinically useful diagnostic markers and potental therapeutic agents for male infertility and cancer. The present oligonucleotide was used in an example from the invention.
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                                                                                                                                                                                                                                                                                   present invention relates to human testis expressed Patched like
                                                                                                                                    Novel isolated human testis expressed Patched like protein (HTPL), useful for identifying agonist and antagonist and specific binding partners, and for treating subjects having defects in HTPL -
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(AEOM-) AEOMICA INC
                                                                                      WPI; 2002-676582/73
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ABS75576/c
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                                                                                                                                                                                                                            one of three new isoforms of human pregnancy associated plasma protein E, hPAPP-E. The products of the invention have abortive and contraceptive activity and can be used for gene therapy or in a vaccine. The nucleic acid, polypeptide encoded by it, or antibody to the polypeptide can be used in pharmaceutical compositions or vaccines for preventing or aborting pregnancy. PAPP-E is used in the antenatal diagnosis of dysgenetic pregnancies. The nucleic acids are used as probes to assess the level of PAPP-E isoform mRNA in chorionic villus samples, and the antibodies can be used to assess the expression levels of PAPP-E isoform antibodies can be used to assess the expression levels of PAPP-E isoform antibodies can be used to assess the configurate of papp-E isoform antibodies can be used to assess the disciplement of preparaties antenatally. This sequence repersents an oligomer used in scanning the human PAPP-E genes described in the disclosure of the invention.
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New isolated nucleic acid encoding an isoform of human pregnancy associated plasma protein E, for preventing or aborting pregnancy
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ID ABS75577 standard; DNA; 25
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Best Local Similarity 100.8
Matches 10, Conservative
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                                dysgenetic pregnancies. The nucleic acids are used as probes to assess the level of PAPP-E isoform mRNA in chorionic villus samples, and the antibodies can be used to assess the expression levels of PAPP-E isoform proteins in chorionic villus samples, to diagnose dysgenetic pregnancies antenatally. This sequence represents an oligomer used in scanning the human PAPP-E genes described in the disclosure of the invention.
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(SHAN/) SHANNON M E.
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100.0%; Score 10; DB 24; Length 25; 100.0%; Pred. No. 1.8e+04;

Best Local Similarity

Query Match

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Mismatches
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(SHAN/) SHANNON M E.
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                                                                       PAPP-E; human; pregnancy associated plasma protein E; abortive; contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis; dysgenetic pregnancy; primer; ss.
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                                             Human PAPP-Ea associated 25-mer SEQ ID 1106.
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Matches 10; Conservative
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(SHAN/) SHANNON M
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Length 25; 0; Indels

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This invention describes a novel isolated nucleic acid that encodes one of three new isoforms of human pregnancy associated plasma protein E, hPAPP-E. The products of the invention have abortive and contraceptive activity and can be used for gene therapy or in a vaccine. The nucleic acid, polypeptide encoded by it, or antibody to the polypeptide can be used in pharmaceutical compositions or vaccines for preventing or aborting pregnancy PAPP-E is used in the antenatal diagnosis of dysgenetic pregnancies. The nucleic acids are used as probes to assess the level of PAPP-E isoform mRNA in chorionic villus samples, and the antibodies can be used to assess the expression levels of PAPP-E isoform proteins in chorionic villus samples, to diagnose dysgenetic pregnancies antenatally. This sequence reperseents an oligomer used in scanning the human PAPP-E genes described in the disclosure of the invention.
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                                                                                                                                                                                                              New isolated nucleic acid encoding an isoform of human pregnancy associated plasma protein E, for preventing or aborting pregnancy
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                                             06-APR-2001; 2001US-0827998.
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(SHAN/) SHANNON M E.
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Best Local Similarity
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                                                                                                       (GUYY/) GU Y.
(SHAN/) SHANNON M
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ABS75582/
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                                                                                                                                                                                      one of three new isoforms of human pregnancy associated plasma protein B, hPAPP-E. The products of the invention have abortive and contraceptive activity and can be used for gene therapy or in a vaccine. The nucleic acid, polypeptide encoded by it, or antibody to the polypeptide can be used in pharmaceutical compositions or vaccines for preventing or aborting pregnancy. PAPP-E is used in the antenatal diagnosis of dysgenetic pregnancies. The nucleic acids are used as probes to assess the level of PAPP-E isoform mRNA in chorionic villus samples, and the antibodies can be used to assess the expression levels of PAPP-E isoform proteins in chorionic villus samples, to diagnose dysgenetic pregnancies antenatally. This sequence reperseents an oligomer used in scanning the human PAPP-E genes described in the disclosure of the invention.
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                                                New isolated nucleic acid encoding an isoform of human pregnancy associated plasma protein E, for preventing or aborting pregnancy
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WPI; 2002-697817/75.
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Best Local Similarity
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used in pharmaceutical compositions or vaccines for preventing or aborting pregnancy. PAPP-E is used in the antendral diagnosis of dysgenetic pregnancies. The nucleic acids are used as probes to assess the level of PAPP-E isoform mRNA in chorionic villus samples, and the antibodies can be used to assess the expression levels of PAPP-E isoform proteins in chorionic villus samples, to diagnose dysgenetic pregnancies antenatally. This sequence represents an oligomer used in scanning the human PAPP-E genes described in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAPP-E, human; pregnancy associated plasma protein E; abortive; contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis; dysgenetic pregnancy; primer; ss.
                                                                                                                                                                                                                                                                                  Gaps
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Best Local Similarity 100.0
Matches 10, Conservative
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(SHAN/) SHANNON M E.
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100.0%; Score 10; DB 24; Length 25;

Query Match

PAPP-E; human; pregnancy associated plasma protein E; abortive; contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis; dysgenetic pregnancy; primer; ss.

06-APR-2001; 2001US-0827998 26-MAY-2000; 2000US-207456P

US2002102252-A1. Homo sapiens.

01-AUG-2002.

SHAN/) SHANNON M E.

(GUYY/) GU

WPI; 2002-697817/75. Gu Y, Shannon ME;

Human PAPP-Ea associated 25-mer SEQ ID 1112.

(first entry)

27-DEC-2002

ABS75586;

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one of three new isoforms of human pregnancy associated plasma protein E, hpapp-E. The products of the invention have abortive and contraceptive activity and can be used for gene therapy or in a vaccine. The nucleic acid, polypeptide encoded by it, or antibody to the polypeptide can be used in pharmaceutical compositions or vaccines for preventing or aborting pregnancy. PAPP-E is used in the antendral diagnosis of dysgenetic pregnancies. The nucleic acids are used as probes to assess the level of PAPP-E isoform mRNA in chorionic villus samples, and the antibodies can be used to assess the expression levels of PAPP-E isoform proteins in chorionic villus samples, to diagnose dysgenetic pregnancies antendatally. This sequence repersents an oligomer used in scanning the human PAPP-E genes described in the disclosure of the invention.
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                          Gaps
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           Pred. No. 1.8e+04;
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                          Mismatches
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100.0%; Pre-
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Best Local Similarity luv...
Local 10; Conservative
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                            10; Conservative
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(SHAN/) SHANNON M E.
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           Best Local Similarity
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New isolated nucleic acid encoding an isoform of human pregnancy associated plasma protein E, for preventing or aborting pregnancy

Example 2; Page 221; 353pp; English

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1 CTICICITII 10 CTTCTCTTTT 7

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ВР.

ABS75586 standard; DNA; 25

ABS75586/c ID ABS7558 XX RESULT 86

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The inversion was come a mover in the contracted plans a protein E, hPAPP-E. The products of the invention have abortive and contraceptive activity and can be used for gene therapy or in a vaccine. The nucleic acid, polypeptide encoded by it, or antibody to the polypeptide can be used in pharmaceutical compositions or vaccines for preventing or aborting pregnancy. PAPP-E is used in the antenatal diagnosis of dysgenetic pregnancies. The nucleic acids are used as probes to assess the level of PAPP-E isoform mRNA in chorionic villus samples, and the antibodies can be used to assess the expression levels of PAPP-E isoform mRNA in chorionic villus samples, and the proteins in chorionic villus samples, to diagnose dysgenetic pregnancies antenatally. This sequence represents an oligomer used in scanning the human PAPP-E genes described in the disclosure of the invention.
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                                                              New isolated nucleic acid encoding an isoform of human pregnancy associated plasma protein E, for preventing or aborting pregnancy
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100.0%; Pred. No. 1.8e+04;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25 BP; 12 A; 3 C; 6 G; 4 T; 0 other;
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                                                                                                                              Example 2; Page 221; 353pp; English.
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SHANNON M E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 89
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100.0%; Pred. No. 1.8e+04;
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ABS75588 standard; DNA; 25
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                                                                                                                                                                 (GUYY/) GU Y.
(SHAN/) SHANNON M E.
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acid, polypeptide encoded by it, or antibody to the polypeptide can be used in pharmaceutical compositions or vaccines for preventing or aborting pregnancy. PAPP-E is used in the antenatal diagnosis of dysgenetic pregnancies. The nucleic acids are used as probes to assess the level of PAPP-E isoform mRNA in chorionic villus samples, and the antibodies can be used to assess the expression levels of PAPP-E isoform proteins in chorionic villus samples, to diagnose dysgenetic pregnancies antenatally. This sequence represents an oligomer used in scanning the human PAPP-E genes described in the disclosure of the invention.
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100.0%; Pred. No. 1.8e+04;
tive 0; Mismatches 0;
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ABS7590/C
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ABS760/
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DB 24; 1
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; Pred. No. 1.8e
0; Mismatches
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   100.0%;
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(SHAN/) SHANNON M E.
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AAQ45398/c
ID AAQ45
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Administration of antisense or triplex forming oligonucleotides which bind polypurine tracts (PPT) may be used in the therapy or treatment of individuals infected with retroviruses or hepadna viruses since in these two families of viruses, two primers are involved in the reverse transcription of viral RNA into double cranded DNA, one of which is a PPT. The antisense or triplex forming oligonucleotides can inhibit the early stages of viral replication by binding to the PPT primer or by binding to PPT reacts in the RNA-DNA hybrid molecule formed after reverse tracts in the RNA-DNA hybrid molecule formed after reverse tracts in the RNA-DNA hybrid molecule formed after reverse transcription of the viral RNA. This oligonucleotide was incubated with an in vitro transcribed 5 end labelled pKJ2 RNA of 134 uncleotides in length to which a 40-mer deoxyribonucleotide complementary to the PPT had been hybridised. The presence of this sequence led to protection of the pKJ2 RNA-DNA hybrid from RNAse H of digestion which would suggest the formation of a triplex. Triplex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vitro by reverse transcriptase in the presence of oligodeoxynucleotides including one which was radioactively labelled. The newly synthesised DNA was terminated at the site of the PPT when
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the triplex was formed and blocked extension. Triplex formation would be expected to interfere with viral replication in vivo. See AAQ45381-Q45417. This is a variant of the sequence described in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                formation was confirmed using a primer extension technique. A primer binding downstream of the PPT was synthesised and extended in
                                                                                                                                                            HIV; human immunodeficiency virus; retrovirus; hepadna virus; reverse transcription; virus replication; inhibition; treatment; therapy; polypurine; triplex; antisense; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antivixal oligomers that bind poly-purine tracts of single-stranded RNA or RNA - DNA hybrids - used to target the early stages of viral replication before double stranded DNA is
                                                                                                                      Oligonucleotide forming triplex with viral polypurine tract.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4; Page 29; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                              93WO-US09300.
                                                                                                                                                                                                                                                                                                                                                                                                                      92US-0954184
                                                          (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (APOL-) APOLLON INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1994-135099/16.
                                                                                                                                                                                                                                                                                                                                                                                                                      29-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                            29-SEP-1993;
                                                                                                                                                                                                                                                                                           WO9407367-A1
                                                       25-MAR-2003
11-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Moelling K;
                                                                                                                                                                                                                                                 Synthetic.
                 AAQ45398;
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The present invention describes nucleic acid molecules which modulate the synthesis, expression and/or stability of a mRNA encoding 1 or more receptors of vascular endothelial growth factor (VEGF). A patient (preferably human) having a condition associated with the level of the fime-like tyrosine kinase 1 (fit-1), kinase insert domain containing receptor (KDR) and/or foetal liver kinase in (fit-1) (e.g. tumour angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be treated by administering the nucleic acid molecule or the expression vector to the patient. AAX67275 to AAX75752 represent specific examples of nucleic acid molecules from the present invention.
                                                                                                                                           Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage; tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease; fme-like tyrosine kinase 1; kinase insert domain containing receptor; foetal liver kinase 1; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              o,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shrimp white spot Bacilliform virus (WSBV) oligonucleotide 158.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 10; DB 18; Length 27; 100.0%; Pred. No. 1.7e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                               Mouse flt-1 VEGF receptor hammerhead ribozyme #771.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 9; Page 178; 218pp; English.
               AAX74299 standard; RNA; 27 BP
                                                                                                                                                                                                                                                                                                                                                             96WO-US17480.
                                                                                                                                                                                                                                                                                                                                                                                            96US-0584040.
95US-0005974.
                                                                                                                                                                                                                                                                                                                                                                                                                                           (CHIR ) CHIRON CORP. (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH62997 standard; DNA; 27
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                                                                              28-JUL-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                             25-OCT-1996;
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                                                                                                                                                                                                                                                                                                                                                                                              11-JAN-1996;
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                                                                                                                                                                                                                                                                                                                              01-MAY-1997
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                                                                                                                                                                                                                                            Synthetic.
                                              AAX74299;
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AAX74299/
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Query Match Best Local Similarity Matches 10; Conserv

100.0%; Score 10; DB 15; Length 27; 100.0%; Pred. No. 1.7e+04;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention provides the primary nucleotide sequence of the WSBV genome (AAH62689), predicted transcript sequences (AAH62689-AAH62839) and encoded proteins (AAG8940-AAG88261) and oligonucleotide sequences (AAH62840-63160) suitable for use as primers or probes. The nucleic acid molecules and proteins of the invention are useful for diagnosis and monitoring viral infection, in screens for antiviral agence and for monitoring viral gene expression or activity during a treatment regimen. The nucleic acid molecules are also useful as antisense constructs to control viral gene expression in infected cells and tissues and to create
                                                                                                                                                                                                                                                                                                                                                                         Primary nucleotide sequence of the shrimp white spot Bacilliform virus (WSBV), useful for producing viral polypeptides that can be used to screen for agents that are useful for treating WSBV infection -
Shrimp white spot Bacilliform virus; WSBV; diagnosis; viral infection; antiviral agent; gene expression; antisense construct; probe; primer; transgenic viral resistant shrimp; ss.
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                                                                                                                                                                                                                                                                                                           Shen
                                                                                                                                                                                                                                        (PENY-) PE CORP NY.
(THIR-) THIRD INST OCEANOGRAPHY STATE OCEANI C A.
(SINO-) SINOGENOMAX CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 27 BP; 5 A; 6 C; 2 G; 14 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP specific lower PCR primer SEQ ID 962.
                                                                                                                                                                                                                                                                                                           He M,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Figure 3; 626pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transgenic viral resistant shrimp.
                                                                                                                                                                                                                                                                                                            Ku X, Yang F, He J, Pham L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH38166 standard; DNA; 27 BP
                                                                                                                                                                           08-NOV-2000; 2000WO-US2888
                                                                                                                                                                                                         99CN-0124717
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Best Local Similarity 100.
                                                                       White spot syndrome virus
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                                                                                                        WO200138351-A2
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                                                                                                                                                                                                          24-NOV-1999;
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                                                                                                                                        31-MAY-2001
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primer extension (SNPE) primers, and the sequences of regions flanking stres of single nucleotide polymorphisms SNPs. The present invention includes kits for determining the presence or absence of a SNP, using the includes kits for determining the presence or absence of a SNP, using the oligonucleotides of the invention. The PCR primers are used to amplify a SNP flanking sequence, the SNPE primer is used as a genotyping primer. The oligonucleotides are useful for genotyping a nucleic acid sample by performing a single-nucleotide primer extension reaction. The oligonucleotides are useful for determining the presence, absence or identity of a SNP and for genotyping nucleic acid samples, for e.g. to assess by association analysis the genotypic dan individual or group of individuals, having a pathological phenotypic trait suspected of being caused by one or more SNPs. Phenotypic trait suspected of being caused by one or more SNPs. Phenotypic trait suspected of being caused by one or more SNPs. Phenotypic trait sinclude disease e.g. agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, familial hypercholesterolaemia, polycystic kidney disease, osteogenesis imperfects and acute intermittent porphyria. Phenotypic traits also include symptoms of or susceptibility to multifactorial disease of which a component is or may be genetic such as autoimmune diseases, including, rheumatoid arthritis, multiple sclerosis, inflammation, cancer, nervous system diseases and infection by pathogenic microorganism. The method is also useful in forensic investigations and paternity analysis. The present sequence represents a PCR primer specific
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human MSF; megakaryocyte stimulating factor; tribonectin; alternative splicing; joint boundary lubricant; O-linked oligosaccharide; osteoarthritis; tribosupplementation; tissue adhesion inhibition; friction coefficient reduction; gene therapy; antiarthritic; osteopathic; reverse transcription-PCR; RT-PCR primer; ss.
                                                                                                                                                                                                              New genotyping oligonucleotide, useful for detecting the presence, absence or identity of single polynucleotide polymorphism in a nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human MSF exon 6 RT-PCR primer, SEQ ID NO:16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                For a human SNP containing DNA sequence.
                                                                                                                                                                                                                                                                                                      Claim 1; Page 54; 83pp; English.
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                                                                                   (ORCH-) ORCHID BIOSCIENCES INC
13-OCT-2000; 2000WO-US28436
                                          99US-0160096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 CTTCTCTTT
                                                                                                                                                                        WPI; 2001-290930/30
                                                                                                                                  Picoult-Newburg L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200064930-A2
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                                          15-OCT-1999;
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                                                                                                                                                                                                                                                                acid sample
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Jay GD;

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The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 orphan receptor, EAR3/COUP-TF-1, the GATA transcription factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP). Inhibition of the repressors removes prevents the production (and consequently increases expression of) genes involved in the production of erythropoietin, granulocyte colony stimulating factor protein and interferon alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human CD36 polymorphism sequence variant oligonucleotide SEQ ID NO:133.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; rat; CD36; SHR; spontaneous hypertensive rat; diagnosis; therapy; screening; polymorphism; variant; detection; mutant; blood; mutation; insulin; glucose metabolism; fatty acid metabolism; catecholamine; malaria; infection; parasite; antiparasitic;
                                                                                                                   Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding mutant CD36 proteins useful for preventing, diagnosing and treating parasitic infections, especially malaria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 10; DB 21;
100.0%; Pred. No. 1.7e+04;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 29 BP; 10 A; 4 C; 9 G; 5 U; 1 other;
                                          McSwiggen J;
                                                                                                                                                                                                            Claim 48; Page 124; 164pp; English.
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                                          Pavco P,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA40663 standard; DNA; 29
(RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-AUG-2000 (first entry)
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Matches 10; Conservative
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AITMAN T J.
SCOTT J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANTON L W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29 CTTCTCTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CTICICITII
                                                                                WPI; 2000-647423/62
                                          Zwick M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200019883-A2.
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17-MAR-1999;
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(AITM/)
(SCOI/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (STAN/)
                                          Blatt L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 98
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                                                                                                                                                                                                                                                                                                                                                                             gene, The Infonectin has a least one villared oligosaccharded lubricating molety and has a polypeptide sequence comprising 1-76 repeats of a motif having at least 50% identity to the sequence KEPAPT repeats of a motif having at least 50% identity to the sequence KEPAPT (AAB29744). The invention also relates to a nucleic acid encoding a human MSF-derived tribonectin; a biocompatible composition comprising a human tribonectin for inhibiting tissue adhesion formation; and a method of diagnosing osteoarthritis or a predisposition to osteoarthritis by meammal, wherein an increased amount of MSF compared to a control indicates the presence of or predisposition to developing osteoarthritis. The tribonectin and DNA encoding it are useful in the treatment of osteoarthritis, where they may be used for lubricating mammalian joints, such as articulating joints of humans, dogs or horses. The tribonectin, when formulated as a membrane, foam, gel or fibre, is useful for inhibiting adhesion between two surfaces such as the injured or trauma, or an artificial device e.g., an orthopsactical insertion of tribonectin may be used in gene therapy. The present sequence represents a tribonectin may be used in gene therapy. The present sequence represents
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                                                                                                                                                                                                                                                                                                                     The invention relates to a human tribonectin which is a product of alternative splicing of the human MSF (megakaryocyte stimulating factor) gene. The tribonectin has at least one O-linked oligosaccharide
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                                                                                                                                                                                                                 Novel tribonectin polypeptide useful as lubricant for treating osteoarthritis, comprises O-linked lubricating moiety
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                                                                                         (RHOD-) RHODE ISLAND HOSPITAL LIFESPAN PARTNER.
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    24-APR-2000; 2000WO-US10953
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Best Local Similarity 100.
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AAF05757;

AAF05757/c RESULT 97

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Gaps

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Length 29; Indels

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concoding mutant CD36 proteins (B). Parasites such as Plasmodium falciparum (the major cause of malaria) are unable to utilise the mutant CD36 proteins (B). Parasites such as Plasmodium falciparum (the major cause of malaria) are unable to utilise the mutant cD36 proteins do not function correctly preventing parasites utilising them to infect cells. The mucleic acids may be used for the recombinant production of mutant CD36 proteins according to standard methodologies. They may be used in this way to prevent and treat parasitic infections that utilise the CD36 protein to infect cells, such as P. falciparum, then utilise the CD36 protein to infect cells, such as P. falciparum, identify modulators of CD36 expression and activity or a patient's CD36 by may be screened to determine whether there are any mutations present that may confer resistance to parasitic infections. The proteins and nucleic acids may also be used to prevent, diagnose and treat diseases associated with defects in insulin action and/or glucose metabolism cand/or fatty acid metabolism and/or catecholamine action in subjects possessing mutations in the CD36 genes AAA40606 to AAA40759, and AAB02515 to AAB02554, respectively which are used in the exemplification of the present
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                                                present invention describes isolated nucleic acid molecules (A)
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                Claim 26; Page 90; 167pp; English.
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AITMAN T J.
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STANTON L W.
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28-DEC-1998;
17-MAR-1999;
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concoding mutant CD36 proteins (B). Parasites such as Plasmodium falciparum (the major cause of malaria) are unable to utilise the mutanted proteins to gain entry to, and infect cells. The mutant CD36 proteins do not function correctly preventing parasites utilising them to infect cells. The nucleic acids may be used for the recombinant production of mutant CD36 proteins according to standard methodologies. They may be used in this way to prevent and treat parasitic infections that utilise the CD36 protein to infect cells, such as P. falciparum, they may be used in this way to prevent and treat parasitic infections that utilise the CD36 protein to infect cells, such as P. falciparum, identify modulators of CD36 expression and activity or a patient's CD36 DNA may be screened to determine whether there are any mutations present concern resistance to parasitic infections. The proteins and nucleic acids may also be used to prevent, diagnose and treat diseases associated with defects in insulin action and/or glucose metabolism and/or fatty acid metabolism and/or catecholamine action in subjects possessing mutations in the CD36 genes AAA40666 to AAA40759, and AAB02515 to AAB025164, represent uncleotide and amino acid sequences in insulin action and and and activity action sin the cused in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human CD36 polymorphism sequence variant oligonucleotide SEQ ID NO:134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                             present invention describes isolated nucleic acid molecules (A)
             Nucleic acids encoding mutant CD36 proteins useful for preventing, diagnosing and treating parasitic infections, especially malaria -
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                                                                       Claim 26; Page 90; 167pp; English
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99US-0270542.
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Matches 10; Conservative
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The present invention describes isolated nucleic acid molecules (A) encoding mutant CD36 proteins (B). Parasites such as Plasmodium falciparum (the major cause of malaria) are unable to utilise the mutated proteins to gain entry to, and infect cells. The mutant CD36 proteins do not function correctly preventing parasites utilising them to function correctly preventing parasites utilising them to forduction of mutant CD36 proteins according to standard methodologies. They may be used in this way to prevent and treat parasitic infections. They may be used in this way to prevent and treat parasitic infections. They may be used to malaria. For example, the protein may be used to determine whether there are any mutations present chantify modulators of CD36 expression and activity or a patient's CD36 DNA may be screened to determine whether there are any mutations present that may confer resistance to parasitic infections. The proteins and nucleic acids may also be used to prevent, diagnose and treat diseases associated with defects in insulin action and/or glucose metabolism and/or fatty acid metabolism and/or catecholamine action in subjects possessing mutations in the CD36 genes AAA40606 to AAA40759, and ABB02515 to AAB02564, represent uncleotide and amino acid sequences represent in the exemplification of the present
                                                                                                           Nucleic acids encoding mutant CD36 proteins useful for preventing, diagnosing and treating parasitic infections, especially malaria
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100.0%; Score 10; DB 21; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 10; Conservative 0; Mismatches 0; Indels
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  Stanton LW;
Scott J,
                                                    WPI; 2000-303596/26
  Aitman TJ,
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/clone lib="Arabidopsis thaliana inserence of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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A Sequence-Indexed Library of Insertion Mutations in the
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmer-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Contact: Joseph R. Ecker
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10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Pax: 858 558 6379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic_DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                   Class: TDNA tagged.
Location/Qualifiers
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A1686998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AI686998.1 GI:4898292
                                                                                                                                                                                                                                                                                                                                                    Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
Arabidopsis thaliana
                                                                                                                                                                                     Arabidopsis Genome
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Best Local Similarity 100.
Matches 10; Conservative
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AI686998
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KEYWORDS
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/organism="Homo sapiens"
/mol_type="mRNA"
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/db_zref="taxon:9606"
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Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.45 kb. Life Technologies catalog #:
11541-018 0 9 12 t
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clone 130b12, forward sequence,
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Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma bruce; (TREU92/14 GUTAT 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Maxing small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
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Hall, N. Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Clone distribution: NCI-CGAP clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
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Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae,
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100.0%; Pred. No. 1.5e+05;
iive 0; Mismatches 0;
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                                                                  www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                    Trace considered overall poor quality Insert Length: 2144 Std Error: 0.00 Seq primer: -40VP from Gibco High quality sequence stop: 1. Location/Qualifiers
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BASE COUNT ORIGIN

RESULT 4 BQ590098/c DEFINITION

à q SOURCE ORGANISM

REFERENCE

JOURNAL COMMENT

TITLE

ACCESSION VERSION KEYWORDS

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AL941390 32 24-OCT-2002
Arabidopsis thaliana T-DNA flanking sequence GK-257B04-014921,
                                                                                                blubl179 32 bp mRNA linear EST 20-JUN-2001
602879191F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5010814 5',
mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue type="tumor, biopsy sample"
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/dev stage="5 months"
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Site 2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

a 5 c
                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 32)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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and Weisshaar,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plate: LLAMI1059 row: e column: 23
High quality sequence stop: 32.
Location/Qualifiers
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    .32
    /organism="Mus musculus"

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/strain="FVB/N-3"
/db_xref="taxon:10090"
/clone="IMAGE:5010814"
                                                                                                                                                                                                                                                            Mus musculus (house mouse)
Mus musculus
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20 CTTCTCTTT 11
CTTCTCTTT 9
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                                                                     RESULT 5
BI081179/c
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TITLE
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/clone lib="MPIZ-ADIS-024-storage root"
/note="Vector: pGWVSPORT6; Site_1: Sal1; Site_2: Not1;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saataucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sal1-Not1, primer sites and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SP6-Sall-CCACGCGTCCG-Sprime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project , local P1: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA" /
/cultivar="KWS2320 (double haploid, monogerm breeding line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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Beta vulgaris
Beta vulgaris
Butayota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Bukaryota, Viridiplantae, Streptophyta, Edicots;
Caryophyllales, Amaranthaceae, Beta.
1 (bases 1 to 29)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
and Radelof,U.
                                                                                                                                                                                                                                                                                                                                                                EST 06-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002) Contact: Weisshaar B
                                                                                                                                                                                                                                                                                                                                                      BQ590098 10-019-T7 MPIZ-ADIS-024-storage root Beta vulgaris cDNA - lone 024-019-019-T7 MFIZ-ADIS-024-storage root Beta vulgaris cDNA - lone 024-019-019 3-PRIME, mRNA sequence.

BQ590098.1 GI:26119681
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                                                                                              Length 28;
                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Farsi veisshaa@mpiz-koeln.mpg.de
Insert Length: 29 Srd Brror: 0.00
Plate: 19 row: 0 column: 19
Seq primer: T7; GTAATACGACTCACTATAGGGC.
Location/Qualifiers
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                                                                                           Score 10; DB 29; Pred. No. 1.5e+05; 0; Mismatches 0;
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/organism="Beta vulgaris"
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/clone="024-019-019"
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Conservative 0;
  /clone="130b12"
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                                                                                              100.0%;
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Matches 10; Conservative
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Best Local Similarity
Matches 10; Conserv
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source

FEATURES

BASE COUNT ORIGIN

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Gaps . 0

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1.33
| organism="Arabidopsis thaliana" |
| organism="Arabidopsis thaliana" |
| mol_type="genomic DNA" |
| fmol_type="genomic DNA" |
| strain="Columbia on "
| strain="Columbia on "
| db xref="taxon:3702" |
| clone="SALK | 15:724.25.30.n" |
| clone | ib="Arabidopsis thaliana TDNA insertion lines |
| note="PCR was performed on Arabidopsis thaliana lines |
| each of which contains one or more TDNA insertion |
| elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 bp mRNA linear EST 25-APR-2002
AU256102 3'-directed mouse cDNA library Mus musculus cDNA clone
BED0007468 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                     This is single pass sequence recovered from the left border of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Generation of expressed sequence tags from mouse brain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Kikuya Kato
Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5589
Fax: 81-743-72-5589
Email: kkato@bs.aist-nara.ac.jp,
URL:http://lovez.aist-nara.ac.jp/BED/index.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037,
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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100.0%; Pred. No. 1.6e+05;
tive 0; Mismatches 0;
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/organism="Mus musculus"
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/tissue type="brain"
/clone_lib="3'-directed
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/db_xref="taxon:10090"
                                                                                                                                                                                             Location/Qualifiers
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Mus musculus
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EST.
                                                                                                 Email: ecker@salk.edu
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Kato, K. and Matoba, R.
                                                                                                                                                                       Class: TDNA tagged
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/Glone="GR-257804-014921"

/Glone="GR-257804-014921"

/Glone="GR-257804-014921"

/Glone="DCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thalaina nuclear genome sequence processed for submission. T-DNA derived sequences were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SALK 115724.25.30.n Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_115724.25.30.n, genomic survey, sequence.
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A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
                                                                                                                                                                                                                                        Direct Submission

Submitted (21-OCT-2002) Weisshaar B., Max-Planck-Institut fuer
Submitted (21-OCT-2002) Weisshaar B., Max-Planck-Institut fuer
Submitted (21-OCT-2002) Weisshaar B., Max-Planck-Institut fuer
Subchtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence is recovered from the left border of the T-DNA. It
indicates an insertion close to or within gene At5942900. The
sequences are generated at the MPI for Plant Breeding Research in
the context of the GABI-Kat project. GABI-Kat is part of the German
Plant Genomics program designated 'GABI'. Information on line
availability can be found at:
http://www.mpiz-koeln.mgg.de/GABI-Kat/,
Location/Qualifiers
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
euromids II, Brassicales, Brassicaceae, Arabidopsis.
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                                                                                                 Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weisshaar, B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics Unpublished a loase 1 to 32)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
  A pipeline for automated high-throughput generation of Fk (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines
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Salk Institute Genomic Analysis Laboratory (SIGnAL)
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/strain="Columbia 0"
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                       GSS 03-OCT-2000
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1M0214105F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC1M0214105 F, genomic survey sequence.
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0214 row: I column: 05
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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Location/Qualifiers
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/clone="UUGC1M0214105"
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84112, USA
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative adarose gelectrophoresis. Vector DNA was prepared from a derivative of pwh02 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
17el: 801 585 506
Fax: 801 585 7177
              GSS 05-OCT-2000
                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I. (bases I to 37)

Dunn,D., Aoyagis I to 37)

Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
AZ514585
1M0361B16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic CORD UUGC1M0361B16 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UJGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G7BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 10; DB 28; Length 37;
Pred. No. 1.6e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0
Plate: 0361 row: B coluun: 16
Seg primer: CGTGTADAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 37.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="UUGCIM0361B16"
                                                                                                                                                                                                                     Mus musculus (house mouse)
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Gaps

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EST 14-APR-1998

Matches

DEFINITION

ACCESSION

VERSION KEYWORDS SOURCE

RESULT 11 AZ613373

g

ORGANISM

REFERENCE

JOURNAL

COMMENT

TITLE

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41 bp DNA linear GSS 02-OCT-2000 1M0129A12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0129A12 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /_note="Organ: breast, Vector: pCMV-SPORT4; Site 1: Sall; Site 2: Not1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.2 kb. Life Technologies catalog #:10985-018"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 41)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 40) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                         og34b06.si NCI CGAP Br7 Homo sapiens cDNA clone IMAGE:1441715 3' similar to TR:Q33575 Q33575 NADH DEHYDROGENASE SUBUNIT 4. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 40;
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                          Indels
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100.0%; Pred. No. 1.6e+05;
M.cmatches 0;
  Pred. No. 1.6e+05;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
unknown library type
Trace considered overall poor quality
Seq primer: -40ml3 fwd. BT from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                  mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.40
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1441715"
/lab_host="DH10B"
/clone lib="NCI_CGAP_Br7"
                          0; Mismatches
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100.08;
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Matches 10; Conservative
                            10; Conservative
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Unpublished
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                                                                                                                             CTTCTCTTT
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  Best Local Similarity
Matches 10; Conserv
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AZ375959/c
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TITLE
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KEYWORDS
SOURCE
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note==Tvector: PWD42rv; Purified genomic DNA from M.
musculus C57BL/G/ (male) was obtained from He Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1) a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                             AZ613373
1M0441M12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0441M12 R, genomic survey sequence.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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0
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Insert Length: 10000 Std Error: 0.00
Plate: 0441 row: M column: 12
Seg primer: CACACAGGAAACAGCTATGACC
          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol type="genomic DNA"
/strain="C57BL/6J"
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High quality sequence stop: 39.
Location/Qualifiers
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/clone="UUGC1M0441M12"
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AZ613373.1 GI:11735563
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Fax: 801 585 7177
Email: ddunn@genet
          10; Conservative
                                                           1 CTTCTCTTT 10
                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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source

FEATURES

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Gaps

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Query Match

BASE COUNT ORIGIN

us-09-335-032-71.oli.rst

JOURNAL

COMMENT

TITLE

FEATURES

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Direct Submission
Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
This sequence was generated from the SP6 end of BAC 64G19. 64G19 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene. Further details:

Action/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC050354 linear GSS 01-APR-2003 01S-236-6-1tc6-G01 UniformMu MuTALL Library Zea mays genomic clone 01S-536-6-1tc6-G01, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
Campus, Hinxton, Cambridgeshire, CBIO 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 61D1. 61D1 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene. Further details: http://www.sanger.ac.uk/Projects/D_rerio/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Danio rerio genomic clone DKEY-64G19, genomic survey sequence
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/db_xref="taxon:7955"
/clone="DKBY-64G19"
/tissue_type="Testis"
/note="vector pindigoBAC-536"
a 9 c 9 g 0 t
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/note="vector pindigoBAC-536"
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                                                                                                                                                                                                                 /mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-61D1"
                                                                                                                                                                                             /organism="Danio rerio"
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Best Local Similarity 100.
Matches 10; Conservative
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CC050354/c
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BX124544/c
LOCUS
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (http://www.jax.org/resources/). The DNA was hydrodynamically sheared by repeated passage through a was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with THE DNA polymerase and THE polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwhs2 (gi|4722114|gb|AF129072.1), a copy.number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xili0-Gold (Stratagene) cells and selected for ampicillin resistance."
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BX120830
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Direct Submission
Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome
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Actinopterygii, Neopterygii; Teleostei; Ostariophysi,
Cypziniformes; Cypzinidae; Danio.
                                                                                Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
University of Utah
Rm. Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone lib="Mouse 10kb plasmid UUGCIM library"/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
              whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0129 row: A column: 12
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db xref="taxon:10090"
/clone="UUGC1M0129A12"
                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 41.
Location/Qualifiers
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GSS 28-JAN-2003

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Gaps

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LOCUS DEFINITION ACCESSION

RESULT 14 BX120830/c

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BASE COUNT ORIGIN

SOURCE ORGANISM

VERSION KEYWORDS

AUTHORS TITLE JOURNAL

REFERENCE

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/Worl type="mRNA"
// Ab xref="taxon:9606"
// Clone="IMAGE:1520002"
// Lissue type="pooled germ cell tumors"
// Lissue type="pooled germ cell tumors"
// Lissue type="pooled germ cell tumors"
// Lissue type="pooled germ cell tumors and was then primed with a modified polylinker; lst strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3
vector. Library is normalized. Library was constructed by Bento Soares and M. Patima Bonaldo. "

10 a 23 c 0 9 16 t
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota. Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 49)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
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                                                                                                                                                                                                                                        Length 45;
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100.0%; Pred. No. 1.6e+05;
tive 0; Mismatches 0;
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Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
1..45
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-68A12"
/tissue_type="Testis"
/note="vector pindigoBAC-536"
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nes 10; Conservative
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/db_xref="taxon.457"
/clone="1018-536-6-1to6-G01"
/clone="1018-536-6-1to6-G01"
/clone="Twetor: TOPO-PCR4; DNA flanking Mu transposon
/note="Twetor: TOPO-PCR4; DNA flanking Mu transposon
insertions in Mu inactive lines were extracted from the
UniformMu maize population by the thermo assymmetric
interlaced PCR (TAIL) protocol using primers specific for
the Mu terminal inverted repeat and a set of 16 arbitrary
primers. Amplicons were size enriched using Sepharose 400
spin columns and cloned into the TOPO PCR4 vector."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquirles: humquery@sanger.ac.uk Unpublished
This sequence was generated from the SP6 end of BAC 68A12. 68A12 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene. Further details:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                         Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.

1 (Sases 1 to 45)
Latshaw,S., Tan,B.C., Settles,A.M. and McCarty,D.R.
Sequence tagged transposon insertions from the UniformMu maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi,
Cypriniformes; Cyprinidae, Danio.

    (bases 1 to 45)

                                                                                                                                                                                                                                                                                         Contact: Donald R. McCarty
Plant Molecular and Cellular Biology Program
University of Florial
PO 110690 Gainesville, FL 32611-0690, USA
Tel: 352-392-1928 x322
Email: drm@ufil.edu
Sequence flanking probable Mu insertion site in UniformMu line:
015-536-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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DKEY-68A12, genomic survey sequence
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Location/Qualifiers
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Zea mays"
/mol type="genomic DNA"
/strain="W22 (ACR, bz1-m9)"
/cultivar="UniformMu"
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Location/Qualifiers
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BX120970
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                                     GI:29465245
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AU102691 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone HBMA230056, mRNA sequence.
                                                  Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplana
Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
seurosids II; Brassicales; Brassicaceae; Arabidopsis.
I (bases I to 49)
Alonso, J. M., Leisse, T. J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db xref="caxon:3702"
/clone="SALK 130198.43.95.x"
/clone="SALK 130198.43.95.x"
/clone="Ib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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o,K., Sakaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Ha
.H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Sukami,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
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                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Pax: 858 558 6379
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100.0%; Pred. No. 1.6e+05;
tive 0; Mismatches 0;
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/strain="Columbia 0"
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EMBO Rep. 2 (5), 388-393 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Class: TDNA tagged.
Location/Qualifiers
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AU102691.1 GI:13552212
   GI:24948818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nil.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/lmage/lmage.html
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                                                                                                                                                                                                                           tg53b02.x1 NCI CGAP Ut1 Homo sapiens cDNA clone IMAGE:2212491 3' similar to WP:F59E12.9 CE11534 ;contains element MER22 repetitive element ;, mRNA sequence.
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1 (bases 1 to 49)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATional Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
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Ancylostoma caninum Bukaryota, Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida; Ancylostomatoidea; Ancylostomatinae; Ancylostomatinae; Ancylostomatinae; Ancylostomatinae; Ancylostomatinae; Ancylostomatinae; Ancylostomatinae; Ancylostomatinae; Dases 1 to 52)
McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T., Dante,M., Martam,Hillier,L., Kucaba,T., Theising,B., Bowers,Y. Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
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pb62cl2.yl Anc caninum L3 serum stim pAMP1 v1 Chiapelli McCarter
Ancylostoma caninum cDNA 5', mRNA sequence.
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2 (bases 1 to 51)
Oh,S., Kingsley,T., Shin,H., Zheng,Z., Chen,H. and Hou,S.
Direct Submission
Submitted (26-MAR-2002) Suwan Oh, NCI-FCRDC, Lab. Of Immunobiology;
                                                                                                                                                                                                                                                      AB082596 51 bp DNA linear GSS 29-OCT-:
Drosophila melanogaster DNA, clone:1(2)SH2 1592, genomic survey
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                     Gaps
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Fuctional Genomics: A P element-mediated gene disruption in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1050 Boyles st., Frederick, Maryland 21702, USA (B-mail:ohsuwan@mail.ncifcrf.gov, Tel:1-301-846-7314,
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/mol type="genomic DNA"
/db Xref="taxon:7227"
/clone=1(2)5H2 1592"
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iive 0; Mismatches 0;
         100.0%; Score 10; DB 29; 100.0%; Pred. No. 1.6e+05;
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicacee; Arabidopsis.

(bases I to 51)
Alonso, J. M., Leisse, T. J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C. J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
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/clone="xxxx: 43368.36.90.x"
/clone="xxxx: 43368.36.90.x"
/clone="lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BZ770334 143268.36.90.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_143268.36.90.x, genomic
             Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: ysuzuki@ims.u-tokyo.ac.jp Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5.-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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This is single pass sequence recovered from the left border
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                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 10; DB 9; Length 100.0%; Pred. No. 1.6e+05;
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/mol_type="genomic DNA"
/strain="Columbia 0"
                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HBMA230056"
/clone="HBMA230056"
/clone lib="Sugano Homo sa
a l0 c 17 g 10
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                                                                                                                                                                   Email: est@watson.wustl.edu
The library was constructed by Brandi Chiapelli and Dr. James
McCarter (bchiapel@watson.wustl.edu & jmccarte@watson.wustl.edu) at
McCarter (bchiapel@watson.wustl.edu & jmccarte@watson.wustl.edu) at
Mushington University, Et. Louis. DNA Sequencing by: Washington
University Genome Sequencing Center St. Louis. Nematodes were
provided by Dr. Prema Arasu of North Carolina State University.
The vector to vector length is 53.
The vector to vector langth is 53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pAMP1 (Gibco); Site 1: Not1; Site 2: Sal1;
The library was constructed by Brandi Chiapelli and Dr.
James McCarter at Washington University, St. Louis. The
CDNA was made by using Dynabead oligo-dI priming (Dynal).
PCR based library using a modified protocol from the
SNART PCR CDNA Synthesis Kit from Clontech. Directionally
cloned into the UDG sites of pAMP1. Nematodes were
provided by Dr. Prema Arasu of North Carolina State
University."
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Anc caninum L3 serum stim pAMP1 v1 Chiapelli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                     Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
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/lab_host="DH10B"
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University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:29170"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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Matches 10; Conservative
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JOURNAL
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ORIGIN

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(http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymcleotide kinase. Adaptor oligomucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pware (4722114)[gh]AP129072.1); a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XII0-Gold (stratagene) cells and selected for ampicillin resistance."
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clome_lib="Mouse_lokb_plasmid_UDGCNM_library."
/note="Wector: PWB4Zlv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at: image.llnl.gov
Plate: LLCM363 row: d column: 23.
Location/Qualifiers
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
Plate: 0050 row: O column: 16
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 52.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic_DNA"
/strain="C57BL/6J"
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Best Local Similarity 100.0
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Gaps

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EST 30-JUL-2001
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 56)
Alonso,J.W., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
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the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html" 15 c 3 g 28 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
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100.0%; Pred. No. 1.6e+05;
tive 0; Mismatches 0;
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                                                                                                                                                       100.0%; Score 10; DB 28; 100.0%; Pred. No. 1.6e+05;
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/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_096733"
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                                                                                                                                                                                       Best Local Similarity 100.
Matches 10; Conservative
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AUTHORS
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                                                                                              /GLODE="INAGE:3682"
/tissue_type="carcinoma, cell line"
/lab host="Hill # (1) plage=resistant)"
/clone lib="Hill # (1) plage=resistant)"
/clone lib="Hill # (25"
/clone lib="NIH # (25")
/clone lib="N
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, eudicotyledons, core eudicots, rosids
jeurosids II; Brassicales; Brassicacee, Arabidopsis.
(bases 1 to 55)
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lines
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A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
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/clone="SALK 050419.22.05.x"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
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Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Fax: 858 538 6379
Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 10; DB 10; Length 55; 100.0%; Pred. No. 1.6e+05;
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/mol type="genomic DNA"
/strain="Columbia 0"
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                      organism="Homo sapiens"
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Class: TDNA tagged
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Gaps

us-09-335-032-71.oli.rst

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/tissue_type="berries"
/dev stage="mixed; 8, 9, 11, 13, 15, 16 weeks daf"
/dev stage="mixed; 8, 9, 11, 13, 15, 16 weeks daf"
/clone_lib="An expressed sequence tag database for abiotic
stressed berries of Vitis vinifera var. Chardonnay"
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
EcoRI; Site_2: XhoI"
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CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: I.M.A.G.E. Consortium, LLNL

DNA Sequencing Dy: Washington University Genome Sequencing Center

Clone distribution: NGI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
Vitacae; Viis;
1 (bases 1 to 57)
                                                                                                                                                               An expressed sequence tag database for abiotic stressed berries of Vitis vinifera var. Chardonnay
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 58)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:29760"
/clone="VVD118G10"
                                                                                                                                                                                                                                                                                                                              MS200, Reno, NV 89557-0014, USA
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BACKWARD: T7 21mer (backward)
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                                                                                                                                                                                                                                              Contact: Cushman JC
Department of Biochemistry
University of Nevada
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AI343303.1 GI:4080509
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Seq primer: T3 20mer
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Homo sapiens
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Best Local Similarity 100.(
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                          Tel: 775-784-1918
Fax: 775-784-1650
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     Vitis vinifera
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: estowatson. wustl.edu
The library was constructed by Brandi Chiapelli and Dr. James
McCarter (bchiapel@wastson. wustl.edu & jmccarte@watson. wustl.edu
ashington University, St. Louis. DNA Sequencing by: Washington
University Genome Sequencing Center St. Louis.
Putative full length read
The vector to vector length is 58
Seq primer: -40RP from Gibbo.
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The library was constructed by Brandi Chiapelli and Dr. James McCarter at Washington University, St. Louis. Though was made by using Dynabead oligoity, St. Louis. The CDNA was made library using a modified protocol from the SMART PCR cDNA Synthesis Kit from Contech. Directionally cloned into the UDG sites of pAMPI. Nematodes were provided by Dr. Warwick Grant of AgRearch, New Zealand (warwick GrantGaglesearch.co.nz)."
                                                                                                                                                                                                                                                                     McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hiller, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and
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kx19c11.y3 Parastrongyloides trichosuri FL pAMP1 v1 Chiapelli
McCarter Parastrongyloides trichosuri cDNA 5', mRNA sequence.
BI322307
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Parastrongyloides trichosuri
Eukaryota: Metazoa; Nematoda; Chromadorea; Rhabditida;
Panagrolalmoidea; Strongyloididae; Parastrongyloides.
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/mol_type="mRNA"
/db_xref="taxon:131310"
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/lab_host="DH10B"
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                                                                                     BI322307.1 GI:15001493
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orientation:
SP6-Sall-CCACGCGTCCG-Sprime-cDNA-polyA-CC-Notl-T7; Note:
SP6-Sall-CCACGCGTCCG-Sprime-cDNA-polyA-CC-Notl-T7; Note:
SPG-Sall-CCACGCGTCCG-Sprime-context of the GABI-Beet project
, local PI: Dr. Katharina Schneider, coordinator: Prof.
Christian Jung; Sequence submission managed by
RZEPD/GABI-Primary database: http://gabi.rzpd.de"
a 8 c 17 g 1 t
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Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Bmail: Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Bmail: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitcomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
Suzuki,Y., Yoshitcomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
a S.-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997)
This clone was obtained from a '5'-end-enriched' cDNA library
constructed by 'Oligo-Capping' method. The coding region starts
from the 50 bp upstream to the 3'-end.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (2020K1, Y. 1 Shihara, D., Sasaki, M., Nakagawa, H., Hata, H., Tsunoda, T., Watanabe, M., Komatsu, T., Ota, T., Isogai, T., Suyama, A. and Sugano
b.schulz@kws.de; cloning sites Sall-NotI, primer sites and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Statistical analysis of the 5' untranslated region of human mRNA using 'Oligo-Capped' cDNA libraries
Genomics 64 (3), 286-297 (2000)
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AU077187 Sugano cDNA library Homo sapiens cDNA clone Zrv61646

Similar to 5'-end region of Mouse mRNA for proteasome Z subunit,
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/db_xref="taxon:9606"
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Matches 10; Conservative
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AZ774339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beta vilgaris

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,

Bukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta,

Caryophylales, Amaranthaceae; Beta.

1 (bases 1 to 58)

1 (bases 1 to 58)

Flexiols R., Schulz B., Weisshar, B., Hennig, S., Steinfath, M.,

Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H. and Radelof, U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes plant J. 32 (5), 845-857 (2002)
Contact: Weisshaar B
ADIS DNA core facility at MPIZ
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//oto="Vector: pCMVSPORT6; Site 1: Sall; Site 2: Not1;
cDNA library from sugar beet, library provided by KWS
Kleinwanziebener Saatzucht AG Binbeck, Germany, contact;
                                                                                                                                                                                                                                                                /clome lib="NCI CGAP Lu25"
/note="Organ: lung; Vector: pAMP1; mRNA made from lung carcinoma tissue, cDNA made by oligo-dT priming.
Directionally cloned. Size-selected on agarose gel, average insert size 500 bp. Primary library, non-amplified.
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                                                                                                                                                                      /clone="IMAGE:2061856"
|/Lissue_type="bronchioalveolar carcinoma"
|/dev_stage="adult"
|/lab_host="DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: SB Std Brror: 0.00
Plate: 23 row: F column: 23
Seg primer: SP6; CATACGATTTAGGTGACACTATAG.
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/lab host="EMDH108"
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                                                                                                    organism="Homo sapiens"
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/clone="024-023-F23"
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                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
                          High quality sequence stop: 1.
                                               Location/Qualifiers
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Seq primer: -40UP from Gibco
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Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|ARL29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampleillin resistance."
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     GSS 16-FEB-2001
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
AZ774339 Strong S9 bp DNA linear GSS 16-FEB-200
2M0003005R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0003005 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Male"
/lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Seg primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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High quality sequence stop: 59.
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                                                                                                                                               Mus musculus (house mouse)
Mus musculus
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RESULT 35

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Arabidogsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

Alonso, J. M., Leisse, T. J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C. J., Parker, H., Prednis, L., Shinn, P. A. Sequence-Indexed Library of Insertion Mutations in the
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Arabidopsis thaliana T-DNA flanking sequence GK-026B10-013759,
   linear GSS 14-NOV-2002
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/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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BZ354535 14-NOV-2 SALK 125268.25.05.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_125268.25.05.x, genomic
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The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Fax: 858 558 6379
Fax: 858 558 6379
Email: ecker@salk.edu
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/mol_type="genomic DNA"
/strain="columbia 0"
/db xref="taxon:3702"
/clone="SALK_125268.25.05.x"
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                                                                                                                                                                          BZ354535.1 GI:24945397
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/wol type="genomic DNA"
/wol type="genomic DNA"
/strain="Columbia o"
/db xref="taxon:3702"
/clone="CR-026B10-013759"
/clone="CR-026B10-013759
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AUZSB677 3'-directed mouse cDNA library Mus musculus cDNA clone
BED0013467 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                Submitted (17-50M-2002) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence is recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by clone F22B13. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the Carman Plant Genomics program designated 'GABI'. Information on line availability can be found at:

Location/Qualifiers
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Kato, K. and Matoba, R. Generation of expressed sequence tags from mouse brain
                                                                                                                    Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weisshaar, B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics
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   flanking sequence tags) from Arabidopsis thaliana T-DNA
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URL:http://love2.aist-naxa.ac.jp/BED/index.html.
                                                                                                                                                                                                                                                                                      Li,Y., Strizhov,N., Rosso,M. and Weisshaar,B. Direct Submission
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Tel: 81-743-72-5581
Fax: 81-743-72-5589
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Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, J
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/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI, Site_2: Xho I; Lymphatic filarial nematode parasite of humans.

MRNA was prepared from young adult worms isolated from the peritoneal cavity of jirds and converted to double-stranded cDNA using reverse transcriptase and oligo (dT) followed by RNase H and DNA pol I. The library has 6.5 x 104 independent recombinants and the average insert size is approx. BODbp. The library was constructed by Michelle Lizotte-Wanlewski. The library is available from Dr. S.A. Williams, email: genome@neal.smith.edu."

a 10 c 18 g 11 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AW874904 64 bp mRNA linear EST 22-MAY-2000 SWYACAL04A01SK Brugia malayi young adult cDNA (SAW99MLW-BmYA) Brugia malayi cDNA clone SWXACAL04A01 5', mRNA sequence.
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Onchocercidae; Brugia.
1 (bases 1 to 64)
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                                                                                                         /tissue type="brain"
/clone lib="3'-directed mouse cDNA library"
11 c 11 g 24 t 1 others
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Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science
College, Northampton, MA, 01063, USA
Tel: 4135853826
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                                                                                                                                                                                                                                                      100.0%; Score 10; DB 9; L 100.0%; Pred. No. 1.6e+05;
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/mol_type="mRNA"
/db_xref=rtaxon:6279"
/clone="SWYACAL04A01"
/dev_stage="young adult"
/lab_host="XL1-Blue MRP'"
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/organism="Mus musculus"
                           /mol_type="mRNA"
/db_xref="taxon:10090"
/clone="BBD0013467"
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Email: genome@smith.edu
Seq primer: pBluescript SK.
Location/Qualifiers
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DEFINITION AW874934/C

RESULT 39

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ACCESSION VERSION KEYWORDS ORGANISM

SOURCE

REFERENCE AUTHORS JOURNAL

TITLE

COMMENT

FEATURES

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/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI, Site_2: Xho I: Filazial nematode parasite of humans. mRNA was prepared from approximately 9,000 L2s isolated from Approximately 9,000 L2s isolated from Lambda Converted to double-stranded cDNA using reverse transcriptase and colgo GT) followed by RNase H and DNA pol I. The library has 7.3 x 10E4 independent recombinants and the average constructed by Michelle Lizotte-Wanlewski. The library is available from Dr.S.A.Williams, email: genome@smith.edu."
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                                                                                          Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
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Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="L2"
/lab_host="XL1-Blue MRF'"
/lone lib="Onchocerca volvulus L2 larvae cDNA
(SAW98WLW-OvL2)"
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                Williams, S.A.
Genes expressed in L2 larvae of Onchocerca volvulus
Unpublished
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/db_xref="taxon:6282"
/clone="SWOvL2CAS08D03"
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Seg primer: pBluescript SK.
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Email: genome@smith.edu
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Williams, S.A.
(bases 1 to 64)
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Email: genome@sr
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                                                                                                                                                                                                                               Tel: 4135853826
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                AUTHORS
TITLE
JOURNAL
COMMENT
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REFERENCE
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Xho I; Lymphatic filarial nematode parasite of humans.

RRMA was prepared from young adult worms isolated from the
peritomeal cavity of jirds and converted to
double-stranded cDNA using reverse transcriptase and
oligo(dT) followed by RNase H and DNA pol I. The library
has 6.5 x 104 independent recombinants and the average
insert size is approx. 800bp. The library was constructed
by Michelle Lizotte-Waniewski. The library is available
from Dr. S.A. Williams, email: genome@neal.smith.edu."

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SWYACAL04D04SK Brugia malayi young adult cDNA (SAW99MLW-BMYA)
Brugia malayi cDNA clone SWYACAL04D04 5', mRNA sequence.
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SWOVL2CAS08D03SK Onchocerca volvulus L2 larvae cDNA (SAM98MLW-OvL2)
Onchocerca volvulus cDNA clone SWOvL2CAS08D03 5', mRNA sequence.
BE239248
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Brugia malayi
Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Brugia.

1 (bases 1 to 64)
Williams, S. A.
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Eukaryota, Metazoa, Nematoda, Chromadorea, Spirurida, Filarioidea,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Sreven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
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Unpublished
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/lab_host="XL1-Blue MRF'"
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/db_xref="taxon:6279"
/clone="SWYACAL04D04"
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Email: genome@smith.edu
Seq primer: pBluescript SK.
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Best Local Similarity 100.
Matches 10; Conservative
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                      34 CTTCTCTTTT 25
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RESULT 40 BE239248/c

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DEFINITION

LOCUS

ACCESSION

KEYWORDS

SOURCE

VERSION

ORGANISM

BASE COUNT ORIGIN

0

Gaps ; 0

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available from Dr.S.A.Williams, email: genome@smith.edu."
                                                                                          100.0%; Score 10; DB 10; Length 64; 100.0%; Pred. No. 1.6e+05; ive 0; Mismatches 0; Indels
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/lab_host="XL1-Blue_MRF'"
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/db_xref="taxon:6282"
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Location/Qualifiers
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Molecular Parasitology
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                                                                                                                                                        /note="Vector: Lambda Uni-ZAP XR; Site 1: Eco RI, Site 2:
Xho I; Filarial nematode parasite of humans. mRNA was prepared from approximately 9,000 Los isolated from infected mosquitoes from Kumba, Cameroon and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 7.3 x 1084 independent recombinants and the average insert size is approximately lkb.The library was constructed by Michelle Lizotte-Waniewski. The library is available from Dr.S.A.Williams, email: genome@smith.edu."
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Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
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/lab_host="XL1-Blue MRF'"
/clone_lib="Onchocerca volvulus L2 larvae cDNA
/AM98MLW-OvL2)"
                                                                                                               /clone lib="Onchocerca volvulus L2 larvae cDNA (SAW98MLW-OvL2)"
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                                                                       /dev_stage="L2"
/lab_host="XL1-Blue_MRF'"
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/db_xref="taxon:6282"
/clone="SWOvL2CAS08H03"
                          db_xref="taxon:6282"
clone="SWOvL2CAS08G03"
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Email: genome@smith.edu
Seg primer: pBluescript SK.
Location/Qualifiers
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  /mol_type="mRNA"
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/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Ahol : Filatial nematode parasite of humans. mRNA was proported from approximately 9,000 L2s isolated from infected mosquitoes from Kumba, Cameroon and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 7.3 x 10E4 independent recombinants and the average insert size is approximately lkb. The library was represented by Michelle Lizotte-Waniewski. The library is available from Dr.S.A.Williams, email: genome@smith.edu."
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Onchocercidae; Onchocerca.
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Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 413583826
Fax: 413585786
Email: genome@smith.edu
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Xho I; Filarial nematode parasite of humans. mRNA was
prepared from approximately 9,000 L2s isolated from
infected mosquitoes from Kumba, Cameroon and converted to
double-stranded cDNA using reverse transcriptase and
oligo (d7) followed by RNase H and DNA pol I. The library
has 7.3 x 1084 independent recombinants and the average
insert size is approximately lkb.The library was
constructed by Michelle Lizotte-Waniewski. The library is
available from Dr.S.A.Williams, email: genome@emith.edu."
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SWOVL2CAS14A09SK Onchocerca volvulus L2 larvae cDNA (SAM98MLM-OvL2) Onchocerca volvulus cDNA clone SWOVL2CAS14A09 5', mRNA sequence.
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Onchocercidae; Onchocerca.
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Onchocercidae; Onchocerca.
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Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
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/lab_host="xll-Blue MRF'"
/SAM98MLN-OvL2)"
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Molecular Parasitology
Smith College Department of Biological Sciences
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 413883826
Fax: 4138853786
Email: genome@smith.edu
Seq primer: pBluescript SK.
Location/Qualifiers
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Matches 10; Conservative
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/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematcde parasite of humans. mRNA was prepared from approximately 9,000 L2s isolated from Forest continued infected mosquitoes from Kumba, Cameroon and convert double-stranded cDNA using reverse transcriptase and club(apply) followed by RNase H and DNA pol I. The library has 7.3 x 1084 independent recombinants and the average insert size is approximately lkb.The library was constructed by Nichelle Lizotte-Waniewski. The library is available from Dr.S.A.Williams, email: genome@smith.edu."
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Eukaryota, Metazoa, Nematoda, Chromadorea, Spirurida, Filarioidea,
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Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Department of Biological Sciences, Clark Science Center, Smith College, Northampton, MA, 01063, USA
Tel: 413853826
Fax: 413885786
Email: genome@smith.edu
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/lab_host="Xl1-Blue MRF'"
/clone lib="Onchocerca volvulus L2 larvae cDNA
(SA098MLW-OvL2)"
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/lab_host="XL1-Blue MRF'"
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                                                                                                                                                                                                                                     /mol type="mRNA"
/db xref="taxon:6282"
/clone="SWOvL2CAS14C02"
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/db_xref="taxon:6282"
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                                                                                                                                       Seq primer: pBluescript SK.
Location/Qualifiers
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/note="Vector: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2:
Xho I; Filarial nematode parasite of humans. mRNA was
prepared from approximately 9,000 L2s isolated from
infected mosquitoes from Kumba, Cameroon and converted to
double-stranded cDNA using reverse transcriptase and
oligo(dT) followed by RNase H and DNA pol I. The library
has 7.3 x 10E4 independent recombinants and the average
insert size is approximately 1kb.The library was
constructed by Michelle Lizotte-Waniewski. The library is
available from Dr.S.A.Williams, email: genome@smith.edu."
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. mRNA was prepared from approximately 9,000 L2s isolated from infected mosquitoes from Kumba, Cameroon and converted to double-stranded CDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 7.3 x 10E4 independent recombinants and the average
                                                                                                                                                                                insert size is approximately lkb.The library was constructed by Michelle Lizotte-Waniewski. The library is available from Dr.S.A.Williams, email: genome@smith.edu." 10 c 14 g 10 t
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Onchocercidae; Onchocerca.
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Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science
College, Northampton, MA, 01063, USA
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/clone="SWOvL2CAS14G07"
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Fax: 4135853786
Email: genome@smith.edu
Seq primer: pBluescript SK.
Location/Qualifiers
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100.0%; Score 10; DB 10; Length 64; 100.0%; Pred. No. 1.6e+05;

100.0%; Pred. ...

10; Conservative

Best Local Similarity Matches 10; Conserve

Query Match

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/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. mRNA was prepared from approximately 9,000 L2s isolated from infected mosquitoes from Kumba, Cameroon and converted to double-stranded cDNA using reverse transcriptase and cligo(dT) followed by RNase H and DNA pol I. The library has 7.3 x 1084 independent recombinants and the average insert size is approximately lkb. The library was constructed by Michelle Lizotte-Waniewski. The library is available from Dr.S.A.Williams, email: genome@smith.edu."
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Onchocercidae; Onchocerca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
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/lab_host="XL1-Blue MRF'"
/clone_lib="Onchocerca volvulus L2 larvae cDNA
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/db_xref="taxon:6282"
/clone="SWOvL2CAS14H03"
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Email: genome@smith.edu
Seq primer: pBluescript SK.
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/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nemarcde parasite of humans. Six adult male worms of Onchocerca volvulus were isolated from consenting patients and quick frozen. Adult male mRNA was converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 2 x 10E5 independent recombinants and the average insert size is ~1100bp. The library was constructed by Michelle Lizotte-Waniewski with worms provided by Dr. Sara Lustigman. The library is available from Dr. Steven A. Williams, email: genome@smith.edu."
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Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocercidae; Onchocerca.

( hases 1 to 64)

Lizotte Waniewski, M. and Williams, S.A.

Genes expressed in adult male stage of Onchocerca volvulus
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Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
                                                                                                                                                                             Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
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/clone_lib="Onchocerca volvulus adult male cDNA
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                                                                                                                                                                                                                                                                                 Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
Seq primer: pBluescript SK.
Location/Qualifiers
                                                                                                                                                          Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Onchocercidae, Onchocerca.
1 (bases 1 to 64)
Williams, S.A.
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Email: genome@smith.edu

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Anotes Wester: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2: Xho I; Filarial nematode parasite of humans. mRNA was prepared from approximately 9,000 L2s isolated from infected mosquitoes from Kumba, Cameroon and converted to double-stranded cDNA using reverse transcriptase and
                                                                                                                                                                                                                                                                   /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filatial nematode parasite of humans. mRNA was propared from approximately 9,000 L2s isolated from infected mosquitoes from Kumba, Cameroon and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by Rnase H and DNA pol I. The library has 7.3 x 10E4 independent recombinants and the average insert aize is approximately lkb. The library was a sonstructed by Michelle Lizotte-Waniewski. The library is available from Dr.S.A.Williams, email: genome@smith.edu."
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SWOVL2CAS13E09SK Onchocerca volvulus L2 larvae cDNA (SAW9BMLW-OvL2)
Onchocerca volvulus cDNA clone SWOvL2CAS13E09 5', mRNA sequence.
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Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
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(SAW98MLW-OvL2)"
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/clone_lib="Onchocerca volvulus L2 larvae cDNA
/SAW98MLW-OvL2)"
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Unpublished
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Seq primer: pBluescript SK.
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1 (bases 1 to 64)
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oligo(dT) followed by RNase H and DNA pol I. The library has 7.3 x 10E4 independent recombinants and the average insert size is approximately 1kb.The library was constructed by Michelle Lizotte-Waniewski. The library is available from Dr.S.A.Williams, email: genome@smith.edu."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Steven A. Williams
Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
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/lab_host="XL1-Blue MRF'"
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tive 0; Mismatches 0;
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/mol_type="mRNA"
/db_xref="taxon:6282"
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Location/Qualifiers
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1 (bases 1 to 64)
Williams, S.A.
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Fax: 4135853786
Email: genome@smith.edu
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Anotes Vector: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2:
Xho I; Filarial nematode parasite of humans. mRNA was
prepared from approximately 9,000 L2s isolated from
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constructed by Michelle Lizotte-Waniewski. The library is
available from Dr.S.A. Williams, email: genome@smith.edu."
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BE636464 Linear EST 25-AUG-2000 SWOVL2CAS13G02SK Onchocerca volvulus L2 larvae cDNA (SAW98MLW-OvL2) Onchocerca volvulus cDNA clone SWOVL2CAS13G02 5', mRNA sequence.
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Bukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
                                                                                                                                                                        Onchocerca volvulus
Onchocerca volvulus
Eukaryota, Metazoa, Nematoda, Chromadorea, Spirurida, Filarioidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
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                                                                                                                                                                                                                                                                                                                                Genes expressed in L2 larvae of Onchocerca volvulus
Unpublished
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/lab_host="XL1-Blue_MRF'"
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/db_xref="taxon:6282"
/clone="SWOvL2CAS13G02"
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Email: genome@smith.edu
Seg primer: pBluescript SK.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Steven A. Williams
                                                                                                                                                                                                                                                                Onchocercidae, Onchocerca.
1 (bases 1 to 64)
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                                                                                                                    BE636464.1 GI:9919491
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Williams, S.A.
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 4135853826
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AUTHORS
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Annual Control of the control of the
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Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
                                                   Molecular Parasitology
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
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1 (bases 1 to 64)
Williams, S.A., Lu, W., Lizotte-Waniewski, M. and Laney, S.J.
Genes expressed in infective third stage larvae of Onchocerca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="Onchocerca volvulus L2 larvae cDNA (SAW98MIM-OvL2)"
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/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Onchocerca volvulus"
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/lab_host="XL1-Blue MRF'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone="SWOvL2CAS13H01"
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/db_xref="taxon:6282"
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Seg primer: pBluescript SK.
Location/Qualifiers
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Email: genome@smith.edu
Seq primer: pBluescript SK.
Location/Qualifiers
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                                      Contact: Steven A. Williams
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Continuous filarial nemacode parasite of humans.

Tho 1; Cutaneous filarial nemacode parasite of humans.

RNA was prepared from third stage infective larvae of conchocerca volvulus isolated from mosquitoes 10 days after infection and converted to double stranded cDNA using reverse transcriptese and oblgo GNT followed by RNase H and DNApol I. The library had 1.8 x 10E5 independent recombinants and average insert size was 900 base pairs. The library was constructed by Wenhong Lu. The library is available from Dr. S.A. Williams, email genome@Smith.edu."

a stage of the stag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anotes Wetcher: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, 13, were isolated from infected black files in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. 13 of 0. volvalus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3
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Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
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1 (bases 1 to 64)
williams S.A., Lizotte-Waniewski,M., Laney,S. and Lustigman,S. Genes expressed in molting L3 larvae of Onchocerca volvulus
                                                                                                                                      /lab_host="XL1-Blue MRF'"
/clone_lib="Onchocerca volvulus infective larva CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 10; DB 10; Length 64; 100.0%; Pred. No. 1.6e+05;
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/strain="Kumba, Cameroons"
/db_xref="taxon:6282"
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/dev stage="molting L3"
/lab_host="XL1-Blue MRF'"
/strain="Sierra Leone"
/db_xref="taxon:6282"
/clone="SWOvL3CAN69E12"
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                                                                                                                                                                                                                                     (SAW94WL-OvL3)"
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Fax: 4135853786
Email: genome@smith.edu
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Matches 10; Conservative
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(SIDSTANTANOVALLE)
(NDCHE="WestCar: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3. were isolated from infected black flies in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of O. volvulus molt to fourth-stage larvae by day 5 in culture. MRNA was isolated from approximately 6000 molting larvae (ML3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded CDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA DOI. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is ~1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams.
in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol 1. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10B6 independent recombinants and the average insert size is ~1200 bp. The Library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams. The Library is available from Dr. Sara Lustigman (email:
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Eukaryota, Metazoa, Nematoda, Chromadorea, Spirurida, Filarioidea,
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Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith College, Northampton, MA, 01063, USA
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100.0%; Pred. No. 1.6e+05;
tive 0; Mismatches 0; Indels 0; Gaps
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/clone="SWOv3MCAM62B04"
/dev_stage="molting L3"
/lab_host="XL1-Blue MRF'"
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Seq primer: pBluescript SK.
Location/Qualifiers
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1 (bases 1 to 64)
Williams, S.A., Lizotte-Wani
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Best Local Similarity 100.0%;
Warches 10; Conservative 0
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Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams.
The library is available from Dr. Sara Lustigman (email:
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1 (bases 1 to 64)
Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S. Genes expressed in molting L3 larvae of Onchocerca volvulus
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SWOv3MCAM62B125K Onchocerca volvulus molting L3 larva cDNA
(SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOv3MCAM62B12 5',
The library is available from Dr. Sara Lustigman (email:
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Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
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Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps
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Pred. No. 1.6e+05;
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/strain="Kumba, Cameroons"
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/lab_host="XL1-Blue MRF'"
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/clone="SWOv3MCAM62B12"
                                   slustigm@nybc.org)."
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Seg primer: pBluescript SK.
Location/Qualifiers
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/note="Wedgeror: Jambda Uni-ZAP XR; Site 1: Eco RI; Site 2:
Xho I; Filarial nematode parasite of humans. Third-stage
larvae, L3, were isolated from infected black files in
cameroon (forest strain). The L3 were cultured in 20% FCS
in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in
culture. L3 of 0. volvulus molt to fourth-stage larvae by
day 5 in culture. mRNA was isolated from approximately
6000 molting larvae (mL3), 2000 larvae from day 1, 2 or 3
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and DNA pol I. The library was constructed in the lambda
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recombinants and the average insert size is -1200 bp. The
library was constructed by Sara Lustigman and Michelle
Lizotte-Waniewski in the Laboratoxy of Dr. S. A. Williams.
The library is available from Dr. Sara Lustigman (email:
slustigm@nybc.org).
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                                                BI142452 64 bp mRNA linear EST 05-JUL-2001 SWOV3MCAM62F12SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOv3MCAM62F12 5',
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2M0094B14F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0094B14 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Steven A. Williams
Molecular Parasicology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith College, Northampton, MA, 01063, USA
Tel: 413583786
Fax: 413583786
Email: genome@smith.edu
Seq primer: pBluescript SK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="molting L3"
/lab.host="XL1-Blue MRF"
/clone lib="Onchocerca volvulus molting L3 larva cDNA
(SL96MLW-OvmL3)"
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100.0%; Pred. No. 1.6e+05;
tive 0; Mismatches 0; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                        Onchocercidae; Onchocerca.

1 (bases 1 to 64)
Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S. Genes expressed in molting L3 larvae of Onchocerca volvulus Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Onchocerca volvulus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/strain="Kumba, Cameroons"
/db_xref="taxon:6282"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                  mRNA sequence.
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                      BI142452/c
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DEFINITION
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RESULT 60
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                                                                                                                                                                                      VERSION
                                                                                                                                                                                                                                            SOURCE
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(NOTCE="Vector: Lambda Uni-TAP KR; Site 1: Eco RI; Site 2: Kho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black files in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of 0. volvulus molt to fourth-stage larvae by day 5 in culture. MRNA was isolated from approximately 6000 molting larvae (mL3), 2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNAse H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x lobe independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michalle Lizotte-Wanniewski in the Laboratory of Dr. S. A. Williams. The library is available from Dr. Sara Lustigman (email: shustigm@nybc.org)."
                                                                                                                                                                                                                                      BI142422 64 bp mRNA linear EST 05-JUL-2001 SWOv3MCAM62D04SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOv3MCAM62D04 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Onchocerca volvulus

Bukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Onchocerca.

1 (Damses 1 to 64)
Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S.
Genes expressed in molting L3 larvae of Onchocerca volvulus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mod_type="mmRNA"
/strain="Kumba, Cameroons"
/db_txref="taxon:6282"
/db_txref="molting L3"
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/lab_host="Yath-Blue MRF"
/clone lib="Onchocerca volvulus molting L3 larva cDNA
(SL96MLW-OvmL3)"
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Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
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  0; Mismatches
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: genome@smith.edu
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Best Local Similarity 100.0
Matches 10; Conservative
10; Conservative
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                                                   1 CITCICITIT 10
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Fax: 4135853786
                                                                                                         30 CTTCTCTTT 21
                                                                                                                                                                                                                                                                                                                         mRNA sequence.
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JOURNAL
COMMENT
Matches
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/derostage="Tgatygotseu".yr"
/dev stage="Tgathygotseu".
/lab_host="DH10B (GeneHog, Invitrogen, Inc.)"
/clone llb="TgRH Tachygotse Norm 7 cDNA Library"
/clone llb="TgRH Tachygotse Norm 7 cDNA Library"
/note="Vector: pBluccript SK-; Site l: EcoRI; Site 2: XhoI;
/Toxoplasma RH strain tachyzoites were grown in human
foreskin fibroblast cultures in vitro. The library was
originally constructed by K.L.Man, Cambridge University.
cDNAs were synthesized from polyA RNAs by oligo d(T)
priming and directionally cloned into the EcoRI to XhoI
sites of the Lambda ZapII vector using the ZAP-cDNA
synthesis kit (Stratagene). The primary cDNA library was
mass excised as phagemid using ExAssist helper phage
(Stratagene). Phagemid Using ExAssist helper phage
(Stratagene). Phagemid Using ExAssist a pool of
highly abundant genes which were derived from short-cycle
PCR of the primary cDNA library. The normalized library
was electroporated into DH10B (GeneHog, Invitrogen, Inc).
WARNING: the library contains a small percentage of cDNAs
derived from the human host cells."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact David Sibley (toxost@borcim.wustl.edu) for further information relating to organism, libraries, or clone availability. Seg primer: -40RP from Gibco.
                                                                                                        Toxoplasma gondii

Poxoplasma gondii

Barkaryota, Alveolata; Apticomplexa; Coccidia; Eimeriida;

Sarcocystidae; Toxoplasma.

1 (bases 1 to 65)

1 (bases 1 to 65)

1 (bases 1 to 65)

Caragi,K., Cole,R., Fogarty,S., Sibley,L.D., Ajioka,J.A., White,M.,

Clifton,S., Pape,D., Marrin,J., Wylie,T., Dante,M., Marra,M.,

Hillier,L., Rucaba,T., Theising,B., Bowers,Y., Gibbons,M., Ritter

S., Maguire,L., Waterston,R. and Milson,R., Ronko,I., Kennedy

Toxoplasma EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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Washington University School of Medicine
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/strain="RH (Type I)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: toxo@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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Mus musculus
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CB030041.1 GI:27726413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Clifton, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
                                                                           Coxoplasma gondii
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory Mouse DNA Resource Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pmApQ2 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli Xillo-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases I to 64)
Bunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly and Wright, D., Weiss, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="E. Coli strain XLJ0-Gold, Tl-resistant, F-" /clone lib="Mouse 10kb plasmid UTGCLM library" /note="Vector: PWD42nv; Purified genomic DNA from M.musculus GFSBL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JESTIVALBEOZ.Y1 TGRH Tachyzoite Norm 7 cDNA Library Toxoplasma gondii cDNA clone TgESTzydl8e02.y1 5', mRNA sequence. CB030041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/strain="C57BL/6J"
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                             Mus musculus (house mouse)
Mus musculus
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Best Local Similarity 100.0
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Fax: 801 585 7177
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/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columba 0"
/db_xref="taxon:3702"
/db_xref="taxon:3702"
/done="SALK 059169-41.80.x"
/clone lib="%krabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
33 a 7 c 14 g 11 t
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                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta; eudicotyledons, core eudicots, rosids; eurosids II; Brassicales; Brassicaceae, Arabidopsis.
                                                                                                                                 Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Joske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J., and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of
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Neoptera; Endopterygota; Diptera; Brachyoera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 10; DB 29; Length 65; 100.0%; Pred: No. 1.6e+05;
                                                                                                                                                                                                                                                                                             Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Pax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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Drosophila melanogaster
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Arabidopsis thaliana
                                                                                                                                                                                                                                                   Arabidopsis Genome
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /Jab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/notes="Vector: PWD421v; Purified genomic DNA from M.
musculus C57BL/G/ (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was bydrodynamically sheared by repeated passage and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gif 4732114) glp AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent B. coli XII0-Gold (Stratagene) cells
and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                        308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
   Mammalia, Euthería, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC179177 65 bp DNA linear GSS 02-MAY-2 SALK 059169.41.80.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_059169.41.80.x, genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0361 row: N column: 14
Seg primer: CGTTGTAAAACGACGGCCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
                                                                                                                                                                                                                                          Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0361N14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 65.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Class: plasmid ends
                              (bases 1 to 65)
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                                                                                                                                                                                                                                                                                                                                                                                              Tel: 801 585 5606
Fax: 801 585 7177
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Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence is recovered from the right border of the T-DNA. It indicates an insertion within the locus defined by clone MGH6. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at:

http://www.mpiz-keeln.mpg.de/GABI-Kat/.
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/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-092H09-01201"
/clone lib="Arabidopsis thaliana T-DNA insertion lines"
/otone TPCR was performed on DNA from Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana
Wakaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
Chuo-ku, Minatojima-minamimachi 2-2-3, Kobe, Byogo 650-0047, Japan (Enail:shayashikodb.riken.go.jp, Tel:81-78-301-3184, Fax:81-78-301-3183)
This clone was isolated from genomic DNA flanking an insertion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana T-DNA flanking sequence GK-092H08-012001,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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0
                                                                                                                                                                                                                                                                                                                                                     /note="flanking P{GaWB} transposon insertion"
                                                                                                        of a Drosophila strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 65;
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Rosso,M., Strizhov,N., Li,Y. and Weisshaar,B.
                                                                                                                                                                              'organism="Drosophila melanogaster"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 10; DB 29;
Pred. No. 1.6e+05;
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                                                                                                                                                                                                      /mol_type="genomic DNA"
/strain="NP1611"
                                                                                                                                                                                                                                                    /db_xref="taxon:7227"
/chromosome="3"
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                                                                                                     the P element vector P{GaWB}
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                /clone="NP1611-5-1"
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GSS.
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100.0%;
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Best Local Similarity
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/db_xref="caxoni3702"
/clone="GK-323001-015951"
/clone="GK-323001-015951"
/clone="Ib="Arabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR ware directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thalaina nuclear genome sequence processed for submission. T-DNA derived sequences were
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Strizhov,N. Li,Y. Rosso,M. and Weisshaar,B.
Direct Submission
Submitted (21-OCT-2002) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence is recovered from the left border of the T-DNA. It
indicates an insertion within the locus defined by clone F9H3. The
sequences are generated at the MPI for Plant Breedong Research in
the context of the GABI-Kat project. GABI-Kat is part of the German
Plant Genomics program designated 'GABI'. Information on line
availability can be found at:
http://www.mgiz-koeln.mgg/de/GABI-Kat/.
plants (T1) which were transformed with the T-DNA from vector pActis. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence IIAhking the insertion. Sequences displaying significant similarity to the A. Halaina nuclear genome sequence processed for submission. T-DNA derived sequences were
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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/strain="Columbia 0"
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W85242.1 GI:1397731
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                                          SOURCE
                                                                                                                                                                                                                                                                                        65 bp DNA linear GSS 13-DEC-2000
T. brucei sheared genomic DNA clone 129a12, forward sequence,
genomic survey sequence.
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Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TRE0927/4 GTTAt 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v+ i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing. A Practical Approach, eds. M. Vaudin and B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Theres I to 65)
Hall N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CBIO 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
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                                                                                                                              Gaps
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Trypanosoma.
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                                                                                      Length 65;
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                                                                                  Query Match 100.0%; Score 10; DB 29; : Best Local Similarity 100.0%; Pred. No. 1.6e+05; Matches 10; Conservative 0; Mismatches 0;
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/strain="TREU927"
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/clone="129a12"
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                        179
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Matches 10; Conservative
      removed"
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T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Uniu', from 2 ]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT7T3 vector. Library went through one round of
Dormalization, and was constructed by Bento Soares and
M Farima Ronald .
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                     Mus musculus

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 66)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., La, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
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/dev_stage="13.5-14.5dpc_total_fetus"
/lab_host="DH108"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                      The WashU-HHMI Mouse EST Project
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:408735"
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Mus musculus (house mouse)
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Glycine max (soybean)
Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pubMed (gqi 4732114 [gb] AR129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                     Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                   Mammalia; Butheria; Rodentia; Sciurognathi; Murinae; Mus. 1 (bases 1 to 66)
                                                                           Duni, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab host="E. Coli strain XLIO-Gold, Tl-resistant, F-" /clone lib="Mouse 10kb plasmid UGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             ddunn@genetics.utah.edu
Length: 10000 Std Error: 0.00
0361 row: K column: 04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plate: 0361 row: K column: 04
Seg primer: CGTTGTAAAACGACGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="CS7BL/6J"
                                                                                                                                                                                                                                                                       Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="UUGC1M0361K04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 66.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AI442885.
AI442885.1 GI:4299305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet
                                                                                                                                                                                                                          plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CTICICITIE 10
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Best Local Similarity
                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                           USA
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ORIGIN
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                                                          REFERENCE
                                                                                   AUTHORS
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                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                         COMMENT
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paper towers with district deader. Stratagene's conva-
Synthesis Kit (catalog #200401) was used to synthesis the
CODA. First- strand synthesis was performed with 5-methyl
dCTP, hence the ligated cDNA is heminethylated.
Stratagene's first-strand synthesis primer was used
CGAGAGAGAGAGACACTACTCCGAG(T)-18]. After
second-strand synthesis, the CDNA ends were 'polished'
with clone Pfu DNA polymerase, ligated to EcoRI adapters,
and phosphorylated. The XhoI site within the first-strand
synthesis primer was restricted by digestion with XhoI;
all XhoI sites in the CDNA would be protected by their
hemimethylated status. The CDNA constructs were
size-fractionated with a 500p cutoff, using GibcoBRL Life
factionated with a 500p cutoff, using GibcoBRL Life
Technologies coDNA Size Fractionation column. The column
eluent was then ligated into Stratagene's pBluescript II
XR Predigested vector (pBluescript II SK(+) that had been
digested with EcoRI and XhoI, and phosphorylated). Both
the white and blue colonies appear to contain recombinant
plasmids with cDNA inserts. Blue colonies 9n=15) have been
sequenced, and possess putative cDNA inserts. This library
was constructed by Dr. Paul Ken & Virginia H. Coryell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone lib="Gm-cl004"
/note="Vector: pBluescript II XR; Site 1: EcoRI; Site 2:
/note="Vector: pBluescript II XR; Site 1: EcoRI; Site 2:
/note="Wector: pBluescript II XR; Site 1: EcoRI; Site 2:
//note="Wector: pBluescript II XR; Site 1: EcoRI; Site 2:
//note="Wector: pBluescript II XR; Site 1: EcoRI; Site 2:
//note="Wector: pBluescript II XR; Site 1: EcoRI; Site 2: EcoRI; Site 2: EcoRI; Site 2: EcoRI; Site 3: EcoRI; Site 3:
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae,
                                                                                                                                                                                                                                                                                                                                              Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillar, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, A. Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Milson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Biology, Box5640, Northern Arizona
University, Flagstaff, Az 86011, Phone: 520-523-1078 (Dr.
Paul Keim), 520-523-1372 (Virginia H. Coryell), Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand This clone is
available through: ResGen, Invitrogen Corp. 2130 South Memorial
Parkway Huntsville, AL 35801 For further information call: (800
5-533 4533 or contact via email: ccu@resgen.com
Seg primer: -400P from Gibco
High quality sequence stop: 1
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'clone="GENOME SYSTEMS CLONE ID: Gm-c1004-592"
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Paul Keim), 520-523-1372 (Virginia H. Cc
520-523-7550, email: paul keim@nau.edu,
virginia.coryell@nau.edu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Glycine max"
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/db_xref="taxon:3847"
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/lab_host="XL10-Gold"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                 (bases 1 to 67)
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Matches

ò g DEFINITION

ACCESSION KEYWORDS SOURCE

VERSION

RESULT 72

CD029241

ORGANISM

REFERENCE AUTHORS

JOURNAL

TITLE

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AL757142 68 bp DNA linear GSS 18-JUN-2002
Arabidopsis thaliana T-DNA flanking sequence GK-118D11-012821,
                                                                                                                                 EST 01-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue type="Cells, which was adapted in 2.5M NaCl via a incremental series from 1.7 to 2.0 to 2.25 to 2.5 M NaCl, were exposed to 3.4 M NaCl for 5 hours."
//cell type="Green" and to a sequence tag database for the haloto-larant green alga, Dunaliella salina."
//note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1: ECORI; Site 2: XhoI; Library construction was performed according to Stratagene's recommended protocol for the Lambda UnizapXR vector and CDNA synthesis kit."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        An expressed sequence tag database for the halotolerant green alga,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                     Duraliella salina
Dunaliella salina
Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
Dunaliellaceae, Dunaliella.
                                                                                                   DSA008D10 57203 An expressed sequence tag database for the halotolerant green alga, Dunaliella salina Dunaliella salina cDNA clone DSA008D10 5, mRNA sequence.

BM447201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .68
/organism="Dunaliella salina"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plate: 008 row: D column: 10
Seq primer: T3 Zoner
High quality sequence stop: 68.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:3046"
/clone="DSA008D10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Department of Biochemistry
University of Nevada
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: jcushman@unr.edu
                                                                                                                                                                                                                                                        BM447291.1 GI:19852863
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Cushman JC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BACKWARD: I7 21mer
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Unpublished
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  23 CTTCTCTTTT 32
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BM447291/c
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KEYWORDS
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/downer="manusons.iggs.com"
/sex="Mat1-2 hermaphrodite"
/sex="Mat1-2 hermaphrodite"
/sex="Mat1-2 hermaphrodite"
/coll type="mycelium"
/clone lib="Magnaporthe grisea NS Uni-Zap XR Library"
/clone lib="Magnaporthe grisea NS Uni-Zap XR Library"
/note="Vector: pBluescriptsK-; Site_1: EcoRI; Site_2: XhoI;
/fute="Vector: pBluescriptsK-; Site_1: EcoRI; Site_2: XhoI
/fute= nature loom library. Cells were incoulated into
minimal medium and grown for two days with shaking (150
/fute= naturested, washed with water and incoulated into
minimal medium base lacking nitrogen source for 6 h.
/fute= naturested into minimal medium was entended was
/fute length alignment to the M. grisea genome sequence was
available, the EST sequence was trimed according to the
alignment, otherwise sequence was trimed according to the
files (0.05) and for vector seqs."
                                                                                                                                                                                                            67 bp mRNA linear EST 07-MAY-2003
grisea cDNA clone mgns007xAl0 5', mRNA sequence.
CD022241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact person
  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ebbole, D.J., Yuan, J., Thomas, T.L., Bobrowicz, P., Lu, G., Bhatterai, K. and Dean, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Expressed sequence tags from the rice blast fungus, Magnaporthe
                                                                                                                                                                                                                                                                                                                                                                                          Magnaporthe grisea (anamorph: Pyricularia grisea)
Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4483
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  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Magnaporthe grisea"
/mol_type="mRNA"
/strain="Guy11"
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BACKWARD: T7 primer
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                                                    1 CTTCTCTTTT 10
                                                                                                   56 CTICICITIT 65
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source

FEATURES

BASE COUNT ORIGIN

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/clone lib="NCI CGAP GCB1"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
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                                                                                                                                                                                                                                                                                                                                                        /dev stage="gastrula (stages 10.5-13 mixed)"
/lab host="Escherichia coli XLI-blue"
/clone lib="XGC-gastrula"
/note="Wector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA was oligo dT primed from 5ug of poly A+ RNĀ from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 70)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2831f07.r1 NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:686821 5' similar to SW:YKU2 YEAST P36042 HYPOTHETICAL 21.2 KD PROTEIN IN TOR2-PAS1 INVERGENIC REGION. ; contains element TAR1 repetitive alement i, mRNA sequence.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 1914 Std Error: 0.00
Seq primer: -28ml3 rev2 ET from Amersham
                   Hinkton, Cambridgeshire, CB10 1SA, UK
Email: tropbcanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TGas036d16.sp6
Sequencing Priner: SF6
First sequence is from a Kenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
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/lab_host="DH10B"
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:686821"
                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:8364"
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Sanger Centre
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/Clone lib="Arabidopsis thaliana T-DNA insertion lines"
/clone lib="Arabidopsis thaliana T-DNA insertion lines"
/clone lib="Arabidopsis thaliana plates (TI) which were transformed with the T-DNA from vector pAC161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thalaina nuclear genome sequence were processed for submission. T-DNA derived sequences were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /U DP mRNA linear EST 13-DEC-2001 mRNA sequence.
AL651716 XGC-gastrula Silurana tropicalis cDNA clone TGas036d16 5', AL651716
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence is recovered from the right border of the T-DNA. It indicates an insertion within the locus defined by clone F27K19. The sequences are generated at the MDI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at:

Location/Qualifiers
                                                                                                                                                                                                                                                      Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                       Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Huckle, Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J.
Sanger Xenopus tropicalis EST project 2001 (10_2001)
Unpublished
                                                                                                                A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines
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Strizhov, N., Li, Y., Rosso, M. and Weisshaar, B.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
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                                                                                                        and Weisshaar, B.
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H45651 10 bp mRNA linear EST 31-JUL-1995 yn97d02.sl Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:176355 3' similar to gb|K01562|HUMCRHY1 Human Ro RNA (rRNA);,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (base1 to 70)
Hilliar,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lemon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,R., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="55-year old"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares adult brain N2b5HB55Y"
/clone_"Organ: brain; Vector: pT773D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Bco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [57]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
Insert Size: 979
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 979 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                    constructed by Bento Soares and M. Fatima Bonaldo." 32\ {\rm c} 0 g 38\ {\rm t}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                          100.0%; Score 10; DB 9; Length 70; 100.0%; Pred. No. 1.6e+05;
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/db_xref="GDB:3838551"
/db_xref="taxon:9606"
/clone="IMAGE:176355"
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Location/Qualifiers
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/Ultivar="mixed background W23/A188/B73"
/wol type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db.xref="latxon:4577"
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/tissue_type="leaf"
/dev_stage="adult"
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/clone_lib="1006 - RescueMu Grid G"
/clone_lib="1006 - RescueMu Grid G"
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/clone_lib="1006 - RescueMu fixed maize Mu transposon
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1006004B08.x1 1006 - RescueMu Grid G Zea mays genomic, genomic
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Tel: 650 723 2227
Fax: 650 725 8221
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Class: transposon-tagged.
Location/Qualifiers
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Matches 10; Conservative
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SALK 142959.51.10.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_142959.51.10.x, genomic
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cells were transformed and then screened on LB plates with ampicillin."
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University of Tokyo
4-6-1, Shirokanedai, Minato-ku, Tokyo 108,
Fax: 81-3-5449-5572
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                                                          100.0%; Score 10; DB 28;
100.0%; Pred. No. 1.6e+05;
iive 0; Mismatches 0;
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Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: yusuke@ims.u-tokyo.ac.jp.
Location/Qualifiers
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/db_xref="taxon:9606"
/map="8p21.3-p22"
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BZ770025/c
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// Molitype="genonic DNA"
// Strain="Columbia 0"
// Strain="Columbia 0"
// Advef="Laxon:3702"
// Clone="SALK 142959.51.10.x"
// Clone="Iba"Arabidopsis thaliana TDNA insertion lines and the contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
28 a 13 c 8 g 22 t
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Mus musculus
Bukaryota, Marazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Merazoa; Chordata; Sciurognathi; Muridae, Murinae; Mus.
1 (bases 1 to 72)
Marra, M. Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Marra, M., Hillier, L., Allen, M., Martin, J., Morris, M., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA184862 107-JAN-1997 muSlb11.rl Soares mouse lymph node NbMLN Mus musculus cDNA clone IMAGE:642909 5' similar to gb:D13315 LACTOYLGLUTATHIONE LYASE
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 71)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jaske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated intron of At5g01600. Class: TDNA tagged.
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WashJ-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                    Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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/organism="Arabidopsis thaliana"
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The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:668790"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.0%;
Matches 10; Conservative 0
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                 /tissue_type="lymph node"
/tissue_type="lymph node"
/dev stage="4 weeks"
/lab host="DHDB"
/clone_lib="Soares mouse lymph node NbMLN"
/clone_lib="Soares mouse lymph node 'Vector: pTT73D=Pac (Pharmacia)
with a modified polylinker; Site 1: Not I; Site 2: Eco RI;
is strand cDNA was primed with a Not I - oligo[dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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Mekaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopais.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics
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This sequence is recovered from the left border of the T-DNA. It
indicates an insertion close to or within gene At2g28150. The
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Strizhov,N., Kosso,M., Li,Y. and Weisshaar,B.
Direct Submission
Submitted (07-MAR-2003) Weisshaar B., Max-Planck-Institut fuer
                 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana T-DNA flanking sequence GK-386H01-018249,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 10; DB 9; Length 72; 100.0%; Pred. No. 1.6e+05; tive 0; Mismatches 0; Indels
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                                                                        Trace considered overall poor quality Seq primer: -28Ml3 rev2 from Amersham High quality sequence stop: 1.
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                                                                                                                                                                               /organism="Mus musculus"
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="IMAGE:642909"
                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                   /mol_type="mRNA"
/strain="C57BL/6J"
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Local 10, Conservative
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/db_xref=_taxon:3702"
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/clone==xGK-386H01-018249"
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/clone==xGK-386H01-018249"
/note==pCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161. The lines contain one or more T-DNA from vector pAC161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thalaina muclear genome sequence were processed for submission. T-DNA derived sequences were
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zr70g04.rl Soares NhHMPu SI Homo sapiens cDNA clone IMAGE:668790 5' similar to contains element PTR7 repetitive element ;, mRNA
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sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 10; DB 29; Length 72; 100.0%; Pred. No. 1.6e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                    /organism="Arabidopsis thaliana"
/mol type="genomic DNA"
/strain="Columbia 0"
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Washington University School of Medicine
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Seg primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 65.
                                                                                                                              availability can be found at:
http://www.mpiz-koeln.mpg.de/GABI-Kat/.
Location/Qualifiers
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Contact: Steven A. Williams
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Matches 10, Conservative
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Best Local Similarity 100.0
Matches 10, Conservative
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AW626514/c
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           /done lib="Soares NhHMPu Sl"
//ore="Organ: mixed (see below); Vector: pT7T3D-Pac
//ore="Organ: mixed (see below); Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eoc RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
NbHPU, and fetal heart NbHH19M) were mixed, and ss dircles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.B. clones 260232-265223,
340488-345479, and 484488-489479."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol type="mRNA"
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/clone="SWYD25CAU11A07"
/dev stage="young adult, twenty five days after infection"
/lab_host="XLI-Blue MRF'"
/clone lib="Bragia malayi young adult day 25 cDNA
(SAN99MLW-BmYD25)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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Unpublished
                                                                                                                                                                                                                                                                                                                                                       Length 73;
                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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Email: genome@smith.edu
Seq primer: pBluescript SK.
Location/Qualifiers
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'lab host="DH10B"
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1 (bases 1 to 73)
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Best Local Similarity 100.
Matches 10; Conservative
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AW497651/c
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/note="Wector: Lambda Uni-ZAP XR; Site 1: Eco RI; Site_2:
/note="Wector: Lambda Uni-ZAP XR; Site]: Eco RI; Site_2:
MRA 1; Lymphatic filarial nematode parasite of humans.
mRNA was prepared from L4s isolated from the peritoneal
cavity of jirds and converted to double-stranded cDNA
singing reverse transcriptase and oligo(df) followed by
RNase H and DNA pol I: The library has 2.7 x 105
independent recombinants and the average insert size is
                                                                                                                                                                                                                                                                               73 bp mRNA linear EST 22-MAR-2000
SWL4CAK10B02SK Brugia malayi L4 cDNA (SAW99MLW-BmL4) Brugia malayi
cDNA clone SWL4CAK10B02 5', mRNA sequence.
AW600116
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Onchocercidae; Brugia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
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  Length 73;
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100.0%; Score 10; DB 9; I 100.0%; Pred. No. 1.6e+05;
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/dev stage="larval stage four"
/lab_host="XL1-Blue MRF'"
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Tel: 4135853826
Fax: 4135853786
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/mol_type="mRNA"
/db_xref="taxon:6279"
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Seg primer: pBluescript SK.
Location/Qualifiers
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/note="Wedger: lambda UniZap XR; Site 1: EcoR I; Site 2: Xho I; Cutaneous filarial nemacode parasite of humans.

RNA was prepared from third stage infective larvae of Onchocerca volvulus isolated from mosquitoes 10 days after infection and converted to double stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNApol I. The library had 1.8 x 10E5 independent recombinants and average insert size was 900 base pairs. The library was constructed by Wenhong Lu. The library is available from Dr. S. Williams, email genome@smith.edu."
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SWYD25CAU14C02SK Brugia malayi young adult day 25 cDNA
(SAW99MLW-BMYD25) Brugia malayi cDNA clone SWYD25CAU14C02 5', mRNA
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Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
                                                                                                                                                                                                                                                                                                                                                   lab host="XL1-Blue MRF""

'clone lib="Onchocerca volvulus infective larva cDNA

(SAW94WL-OvL3)"
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Unpublished
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/clone="SWOvL3CAN66D01"
                                                                                                                                                                                                                                                       /mol_type="mRNA"
/strain="Sierra Leone"
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/db_xref="taxon:6279"
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Email: genome@smith.edu
Seq primer: pBluescript SK.
Location/Qualifiers
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Location/Qualifiers
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1 (bases 1 to 73)
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RNA was prepared from third stage infective larvae of Onchocerca volvulus isolated from mosquitoes 10 days after infection and converted to double stranded CDNA using acter transcriptease and oligo(df) followed by Rnase H and DNApol I. The library had 1.8 x 10E5 independent recombinants and average insert size was 900 base pairs. The library was constructed by Wenhong Lu. The library is available from Dr. S.A. Williams, email genome@smith.edu."
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Onchocercidae, Onchocerca.
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                                                                                                                                                                                                                                                                          Unpublished
Contact: Steven A. Williams
Molecular Parasitology
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
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/clone_lib="Onchocerca volvulus infective larva cDNA
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                                                                                                                                                                                                Williams, S.A., Lu, W., Lizotte-Waniewski, M. and Laney, S.J. Genes expressed in infective third stage larvae of Onchocerca
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/clone="SWOvL3CAN64C12"
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/strain="Sierra Leone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: genome@smith.edu
Seq primer: pBluescript SK.
Location/Qualifiers
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Molecular Parasitology
                                                                                                                                                      Onchocercidae, Onchocerca.
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                            AW626514.1 GI:7342379
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Matches 10; Conservative
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                                                       Note="Vector: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2: Xho I; Lymphatic filarial nematode parasite of humans. mRNA was prepared from young adult worms isolated from the peritoneal cavity of jirds on day 25 after infection and converted to double-stranded cDNA using reverse transcriptes and oligo(dr) followed by RNasa H and DNA pol I. The library has 6.2 x 105 independent recombinants and the average insert size is approx.1101bp. The library was constructed by Michelle Lizotte Wanlewski. The library is available from Dr. S.A. Williams, email:
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Eukaryota, Metazoa, Nematoda, Chromadorea, Spirurida, Filarioidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BG310475 1inear EST 23-FEB-200 SWOV3MCAM55G11SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOV3MCAM5G11 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
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1 (Dases 1 to 73)

Williams, S. A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S. Genes expressed in molting L3 larvae of Onchocerca volvulus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
/clone_lib="Brugia malayi young adult day 25 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 10; DB 9; Length 73; 100.0%; Pred. No. 1.6e+05;
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|mol_type="mRNRA"
|strain="Kumba, Cameroons"
|db_xref="taxon:6282"
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/dev_stage="molting L3"
/lab_host="XL1-Blue MRF'"
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Location/Qualifiers
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                                             (SAW99MLW-BmYD25)"
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BG310475.1 GI:13112333
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SOURCE

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/note="Vector: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2: Xho I; Lymphatic filarial nematode parasite of humans.—
mRNA was prepared from young adult worms isolated from the peritoneal cavity of jirds and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 6.5 x 104 independent recombinants and the average insert size is approx. 800bp. The library was constructed by Michelle Lizotte-Waniewki. The library is available from Dr. S.A. Williams, email: genome@neal.smith.edu."
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Uni-Zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is ~1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams. The library is available from Dr. Sara Lustigman (email:
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/lab_host="XL1-Blue_MRF""
/clone_lib="Brugia malayi young adult cDNA (SAW99MLW-BmYA
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Eukaryota, Metazoa, Nematoda, Chromadorea, Spirurida, Filarioidea,
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Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
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/db_xref="taxon:6279"
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                                                                                                                 slustigm@nýbc.org).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Steven A. Williams
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Email: genome@smith.edu
Seq primer: pBluescript SK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Williams, S.A.
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Xho I; Filarial nematode parasite of humans. mRNA was
prepared from approximately 9,000 L2s isolated from
infected mosquitoes from Kumba, Cameroon and converted to
double-stranded cDNA using reverse transcriptase and
oligo(dT) followed by RNase H and DNA pol I. The library
has 7.3 x 10E4 independent recombinants and the average
insert size is approximately lb. The library was
constructed by Michelle Lizotte-Waniewski. The library is
available from Dr.S.A.Williams, email: genome@smith.edu."
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                                                                          BE420470 173 bp mRNA linear EST 24-JUL-2000 SWOVL2CAS09D05SK Onchocerca volvulus L2 larvae cDNA (SAW98MLW-OvL2) Onchocerca volvulus cDNA clone SWOVL2CAS09D05 5', mRNA sequence.
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Onchocerca volvulus cDNA clone SWOvL2CAS09D06 5', mRNA sequence.
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Onchocercidae; Onchocerca.
1 (bases 1 to 73)
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Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
                                                                                                                                                                                                                                                                                                                                           Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
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/lab_host="XL1-Blue MRF'"
/clone_lib="Onchocerca volvulus L2 larvae cDNA
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/db_xref="taxon;6282"
/clone="SWOvL2CAS09D05"
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Seg primer: pBluescript SK.
Location/Qualifiers
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1 (bases 1 to 73)
Williams, S.A.
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Email: genome@sr
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/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Ano I; Filarial nemarode parasite of humans. mRNA was propred from approximately 9,000 i2s isolated from infected mosquitoes from Kumba, Cameroon and converted to double-stranded cDNA using reverse transcriptes and oligo(dT) followed by RNase H and DNA pol I. The library has 7.3 x 10E4 independent recombinants and the average insert size is approximately lkb. The library was a proximately lkb. The library is available from Dr.S.A.Williams, email: genome@smith.edu."
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                                            Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 413585382
Fax: 4135853786
Bmail: genome@smith.edu
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Molecular Paramitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
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/lab_host="Xil-Blue MRF'"
/lone lib="Onchocerca volvulus L2 larvae cDNA
(SAW98MIW-OvL2)"
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Unpublished
Genes expressed in L2 larvae of Onchocerca volvulus
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/mol_type="mRNA"
/db xref="taxon:6282"
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/db_xref="taxon:6282"
/clone="SWOvL2CAS09D06"
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Seg primer: pBluescript SK.
Location/Qualifiers
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Williams, S.A.
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Nonce "W-Cours, lambda Unizap XR; Site 1: EcoR I; Site 2: Xho I; Cutaneous filarial nematode parasite of humans. mRNA was prepared from third stage infective larrae of noncoerca volvulus isolated from mosquitoes 10 days after infection and converted to double stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNAPOI I. The library had 1.8 x 10ES independent recombinants and average insert size was 900 base pairs. The library was constructed by Wenhong Lu. The library is available from Dr. S.A. Williams, email genome@smith.edu."
                                                                                                                                                                                                                                                                                                                                      linear EST 13-NOV-2000
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Onchocercidae; Onchocerca.
1 (bases 1 to 73)
Williams, S.A., Lu, W., Lizotte-Waniewski, M. and Laney, S.J.
Genes expressed in infective third stage larvae of Onchocerca
                                                                                                                                                                                                                                                                                                                                BF228818 SWOVL3CAN76D10SK Onchocerca volvulus infective larva cDNA (SAM94WL-CvL3) Onchocerca volvulus cDNA clone SWOvL3CAN76D10 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Steven A. Williams
Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
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/lab_host="XL1-Blue_MRF'"
/clone_lib="Onchocerca_volvulus_infective_larva_CDNA
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                                                   Length 73;
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100.0%; Pred. No. 1.6e+05;
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/strain="Sierra Leone"
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Fax: 4135853786
Email: genome@smith.edu
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                                      Query Match
Best Local Similarity 100.0
Matches 10, Conservative
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                                                                                                                    /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Kho I; Filatial nematode parasite of humans. mRNA was proproximately 9,000 L2s isolated from infected mosquitoes from Kumba, Cameroon and converted to double-stranded cDNA using reverse transcripteas and oligo(dT) followed by RNase H and DNA pol I. The library has 7.3 x 1064 independent recombinants and the average insert size is approximately LNA. The library was rinsert size is approximately LNA. The library is available from Dr.S.A.Williams, email: genome@smith.edu."
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Smith College Department of Biological Sciences
Smith College Department of Sciences Clark Science Center, Smith College, Northampton, MA, 01063, USA
Tel: 413582398
Fax: 4135823786
Email: genome@smith.edu
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/mol_type="mRNR"
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                     /dev_stage="L2"
/lab_host="XL1-Blue_MRF'"
/clone_lib="Onchocerca_volvulus_L2_larvae_cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 10; DB 10; Length 73; Best Local Similarity 100.0%; Pred. No. 1.6e+05; Matches 10; Conservative 0; Mismatches 0; Indels
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/clone="SWOvL2CAS09F04"
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Location/Qualifiers
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1 (bases 1 to 73)
Williams, S.A.
                                                                                                    (SAW98MLW-OvL2)"
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/organism="Arabidopsis thaliana"

mol_type="genomic DNA"

/srain="Columbia 0"
/strain="Columbia 0"
/db xref="taxxon:3702"
/clone="SALK 024363.42.35.x"
/clone="SALK 024363.42.35.x"
/clone="FCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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(Dases 1 to 75)

(Dases 1 to 75)

(Date, Martin, J., Wylie, T., Dance, D., Martin, J., Wylie, T., Dance, M., Marra, M., Hillier, L., Kucaba, T., Thaising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Peraklin, C., Tasgaraishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K. Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and
Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta, Nagnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 74)
Alonso, J. M., Leisse, T. J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C. J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J. R.
A Sequence-Indexed Library of Insertion Mutations in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At5956780.
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 10; DB 29; Length 74; 100.0%; Pred. No. 1.6e+05;
                                                                                                                                                                                                                                                                                                            Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGnAL) The Salk Institute Genomic Analysis Laboratory (SIGnAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA FIRS, 1888 558 4100 X1752 Fax: 988 558 658 678 Fax: Bmail: ecker@salk.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BZ660902 1-JAN-2003 SALK 024363.42.35.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_024363.42.35.x, genomic
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        SWOV3MCAM64D11SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOv3MCAM64D11 5',
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/lab.host="XL1-Blue MRF"
/Cloime lib="Onchocerca volvulus molting L3 larva cDNA
(SL96MLW-OvmL3)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
                                                                                                                                                                                                                                                                                                         Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S. Genes, expressed in molting L3 larvae of Onchocerca volvulus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/strain="Kumba, Cameroons"
/db_xref="taxon:6282"
/clone="SWOv3MCAM64D11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              slustigm@nybc.org)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: genome@smith.edu
Seq primer: pBluescript SK.
Location/Qualifiers
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                                                                                                                      CB886667.1 GI:30088462
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hes 10; Conservative
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Williams, S.A., Liz
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 4135853826
                                                                 mRNA sequence.
CB886667
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1 (bases 1 to 76)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylle,T., Lennon,G., Soaree,B., Wilson,R. and
Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Soares_mammary_gland_NbMMG"
/note="Organ: mammary_gland; Vector: pT7T3D-Pac (Pharmacia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST 07-0CT-1997
                                                                                     Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalía, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA615345 107-OCT-1995 wRNA linear EST 07-OCT-1995 vo61d12.rl Soares_mammary_gland_NbMMG Mus musculus cDNA clone IMAGE:1054391 5' similar to SW:TRFE_RAT P12346 SEROTRANSFERRIN ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL , contact the IMAGE Consortium (info@image.llnl.gov) for further information.
insert libraries for whole genome shotgun sequencing projects. Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Marra M/Mouse EST Project
Washl-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 10; DB 29; Length 75; 100.0%; Pred. No. 1.6e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Possible reversed clone: Similarity on wrong strand Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                       /organism="Trypanosoma brucei"
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/dev stage="4 weeks"
/lab_host="DH108"
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                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/strain="TREU927"
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/db_xref="taxon:10090"
/clone="IMAGE:1054391"
                                                                                                                                                                                                                                                                                                                          /db xref="taxon:5691"
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                                                                                                                                                                                                                                                                                                                                                     /clone="77c02"
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                                                   Email: est@watson.wustl.edu
The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. Oligo(dT)-SL1 PCR based library. Embryo coDA PCR products of size >400 mucleotides containing SL1 on the 5' end and oligo(dT) on the 3' end were non-directionally cloned into pCRII-TopO(Invitrogen) following the Topo TA cloning protocol. 30-60 cell embryo material was provided by Dr. Richard Davis of City University of New York Graduate Center (redavis@postbox.csi.cuny.edu).

College of Staten Island, Staten Island, NY (redavis@postbox.csi.cuny.edu).

Putative full length read
The vector to vector length is 82
Seq primer: SL1 primer.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /close libe.Ascaris suum embryo SLI TOPO v1"
/close libe.Ascaris suum embryo SLI TOPO v1"
/close libe.Ascaris suum embryo SLI TOPO v1"
Site 2: EcoRI; The library was constructed by Claire
Murphy and Dr. James McCarter at Washington University,
Murphy and Dr. James McCarter at Washington University,
St. Louis. Oligo(dT) -SLI PCR based library. Embryo cDNA
PCR products of size >400 nucleotides containing SLI on
the 5' end and oligo(dT) on the 3' end were
non-directionally cloned into PGAII-TOPO(INVitrogen)
following the Topo TA cloning protocol. 30-60 cell embryo
material was provided by Dr. Richard Davis of City
University of New York Graduate Center, College of Staten
Island, Staten Island, NY (redavis@postbox.csi.cuny.edu)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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T. brucei sheared genomic DNA clone 77c02, forward sequence,
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Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Hall,N., Bowman,S., Lennard,N.J., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:6253"
/dev_stage="30-60 cell embryo"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Ascaris suum"
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Matches 10; Conservative
                              Fax: 314 286 1810
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US-09-107-532A-1937 Sequence 19: 5217891-6 Fatent NO. 55: 17891-6 US-09-238-111-289 Sequence 23: US-08-591-789A-22 Sequence 22: US-09-062-451-22 Sequence 22: US-09-062-451-22 Sequence 22: US-09-598-326-222 Sequence 22: US-09-598-326-222	US-09-289-198-222 Sequence 22: US-08-671-548C-39 Sequence 39 US-08-671-548C-45 Sequence 45 US-08-671-548C-45 Sequence 45: US-09-702-703-71332 Sequence 13:	US-09-736-457-1332 Sequence 15 US-09-736-457-1332 Sequence 15 US-09-736-457-1536 Sequence 15 US-09-328-111-155 Sequence 15	US-09-385-982-446 Sequence 44 US-09-221-0178-1021 Sequence 10 US-09-385-982-239 Sequence 23	US-08-182-042B-3 Sequence 3, US-08-174-465D-1 Sequence 1, us-09-174-465D-1 Sequence 1, us-09-500-5043x-1	US-09-328-111-204 Sequence 20 US-09-328-111-204 Sequence 20 US-09-328-111-602 Sequence 50	US-09-328-111-93 Sequence 10 US-09-227-357-104 Sequence 10	US-09-107-532A-1567 Sequence 15 US-09-539-333D-114 Sequence 11 US-09-3705-3705-37	US-09-107-532A-1927 Sequence 7:	US-09-620-312D-950 Sequence 99 US-08-961-527-376 Sequence 37	US-09-303-09-09-09-09-09-09-09-09-09-09-09-09-09-	US-09-134-001C-2805 Sequence 23 US-09-129-030-35 Sequence 33 US-09-669-751-79 Sequence 73	US-08-791-115B-13 Sequence 1 US-09-140-749-24 Sequence 2	US-09-328-352-2378 Sequence Z. US-09-107-532A-3648 Sequence 3. IIS-09-378-352-2442 Sequence 2.	US-09-996-243-145 Sequence 1 US-08-090-526-3 Sequence 3	US-08-486-715-3 Sequence 3 US-08-486-719-3 Sequence 3 HTC 00.271-254.2	US-08-2/1-554-5 US-08-476-100-3 Sequence 3	US-08-55-861-3 Sequence 3	PCT-US94-07658-3 Sequence 3 US-08-537-400-15 Sequence 1	US-08-706-702-17 Sequence 1 US-08-706-706-17 Sequence 1	US-09-238-4/1-1/ Sequence 1 US-09-461-697-193 Sequence 1	US-09-461-697-191 US-09-107-532A-2425 Sequence 2	US-09-662-250A-13 Sequence 1 US-09-107-532A-3372 Sequence 3	US-09-461-697-189 Sequence 18	US-08-153-848-35 Sequence 35	US-08-722-349-4 Sequence 4, US-09-204-328-4 Sequence 4,	US-09-299-843A-35 Sequence 3	US-09-107-532A-3104 Sequence 3: PCT-US93-11153-35 Sequence 3: US-08-680-395-2
4 US-09-107-532A-1937 Sequence 19: 6 5217891-6 Sequence 28: 8 5217891-6 Sequence 28: 9 US-08-671-548C-33 Sequence 28: 9 US-08-991-789A-222 Sequence 22: 9 US-08-991-789A-222 Sequence 22: 9 US-09-052-4251-222 Sequence 22: 9 US-09-598-326-222	4 US-09-289-198-222 Sequence 22: 4 US-08-671-548C-39 Sequence 39 4 US-08-671-548C-45 Sequence 45 4 US-09-702-703-1332 Sequence 13:	4 US-09-736-457-1332 Sequence 15 4 US-09-736-457-1536 Sequence 15 3 US-09-328-111-155 Sequence 15	3 US-09-385-982-446 Sequence 44 4 US-09-221-0178-1021 Sequence 10 3 US-09-385-982-239 Sequence 23 5 US-09-2030-239 Sequence 23	2 US-08-1482-842B-3 Sequence 3, 3 US-09-174-465D-1 Sequence 1, 465D-1	3 US-09-328-111-204 Sequence 20 3 US-09-328-111-204 Sequence 20 3 US-09-328-111-602 Sequence 50	4 US-09-10/-102-A-2030 Sequence 37 US-09-227-357-104 Sequence 10	4 US-09-107-532A-1567 Sequence 15 4 US-09-539-33D-114 Sequence 17	4 US-09-107-532A-1927 Sequence 1:	4 US-09-620-312D-950 Sequence 99 4 US-08-961-527-376 Sequence 3	4 US-09-1318-931-262 Sequence 24 US-09-215-681-262 Sequence 2	4 US-09-134-001C-2805 Sequence 23 US-09-129-030-35 Sequence 33 US-09-669-751-79 Sequence 73	3 US-08-791-115B-13 Sequence 1 4 US-09-140-749-24 Sequence 2	4 US-09-328-352-2378 sequence Z. 4 US-09-107-532A-3648 sequence Z. 1 TIS-09-32R-352-2442 Sequence Z.	4 US-09-996-243-145 Sequence 1 1 US-08-090-526-3 Sequence 3	1 US-08-486-715-3 Sequence 3 US-08-486-719-3 Sequence 3 1 US-08-486-719-3 Sequence 3 1 US-08-719-719-719-719-719-719-719-719-719-719	1 US-08-2/1-334-3 Sequence 3	2 US-08-565-861-3 Sequence 3 US-08-475-749-3 Sequence 3	5 PCT-US94-07658-3 Sequence 3 2 US-08-537-400-15 Sequence 1	2 US-08-706-702-17 Sequence 1 3 US-08-706-17 Sequence 1	4 US-09-238-4/1-1/ Sequence 1 3 US-09-461-697-193 Sequence 1	3 US-09-461-697-191 Sequence 1 4 US-09-107-532A-2425 Sequence 2	4 US-09-662-250A-13 Sequence 1 4 US-09-107-532A-3372 Sequence 3	3 US-09-461-697-189 Sequence 18	1 US-08-153-848-35 Sequence 35	2 US-08-722-349-4 Sequence 4, 3 US-09-204-328-4 Sequence 4,	3 US-09-299-843A-35 Sequence 3	4 US-09-107-532A-3104 Sequence 3: 5 US-08-11153-35 Sequence 3: 2 US-08-680-395-2 Sequence 2:
US-09-107-532A-1937 Sequence 19: 5217891-6 Fatent NO. 55: 17891-6 US-09-238-111-289 Sequence 23: US-08-591-789A-22 Sequence 22: US-09-062-451-22 Sequence 22: US-09-062-451-22 Sequence 22: US-09-598-326-222 Sequence 22: US-09-598-326-222	100.0 578 4 US-09-289-198-222 Sequence 22: 100.0 582 4 US-08-671-548C-39 Sequence 39 100.0 582 4 US-08-671-548C-45 Sequence 45 Sequence 13: 100.0 591 4 US-09-702-703-705-705-705-705-705-705-705-705-705-705	100.0 591 4 US-09-702-703-1330 Sequence 15.0 100.0 591 4 US-09-736-457-1332 Sequence 15.0 100.0 594 3 US-09-328-111-155 Sequence 15.0 100.0	100.0 599 3 US-09-385-982-446 Sequence 44 100.0 604 4 US-09-221-0178-1021 Sequence 10 100.0 607 3 US-09-385-982-239 Sequence 23	100.0 615 3 US-09-174-465D-1 Sequence 1, 100.0 615 3 US-09-174-465D-1 Sequence	100.0 621 3 US-09-298-1012 Sequence 26 100.0 621 3 US-09-128-111-204 Sequence 66 100.0 621 3 US-09-128-111-602 Sequence 66 100.0 621 3 US-09-128-111-602 Sequence 66 100.0 621 3 US-09-128-111-602	100.0 627 3 US-09-128-111-93 Sequence 100.0 627 4 US-09-227-357-104 Sequence 10	100.0 636 4 US-09-107-532A-1567 Sequence 1: 100.0 642 4 US-09-539-3310-114 Sequence 1: 1.0.0 642 4 US-09-539-3310-114 Sequence 1: 1.0.0 642 4 US-09-708-706-70	100.0 642 4 05-09-736-457-77 Sequence 7: 100.0 642 4 US-09-136-457-77 Sequence 1: 100.0 642 4 US-09-107-532A-1927 Sequence 1:	100.0 648 4 US-09-620-312D-950 Sequence 91 100.0 648 4 US-08-961-527-376 Sequence 3	100.0 650 4 US-09-213-262 Sequence 20.00.0 650 4 US-09-215-681-262 Sequence 20.00.0 650 4 US-09-215-681-262 Sequence 20.00.0 650 4 US-09-215-681-262	100.0 660 4 US-09-134-001C-2805 Sequence 22 100.0 662 3 US-09-129-030-35 Sequence 31 00.0 662 4 US-09-669-751-79 Sequence 7.00 660 4 US-09-669-751-79	100.0 670 3 US-08-791-115B-13 Sequence 1. 100.0 670 4 US-09-140-749-24 Sequence 2.	100.0 678 4 US-09-328-352-2378 sequence 2. 100.0 678 4 US-09-107-5328-3648 Sequence 3. 100.0 678 4 IS-09-328-352-2442 Sequence 2.	100.0 688 1 US-09-996-243-145 Sequence 1 100.0 688 1 US-08-090-526-3	100.0 688 1 US-08-486-715-3 Sequence 3 100.0 688 1 US-08-486-719-3 Sequence 3	100.0 688 1 US-08-2/1-554-5 Sequence 3	100.0 688 2 US-08-565-861-3 Sequence 3 100.0 688 3 US-08-475-749-3 Sequence 3	100.0 688 5 PCT-US94-07658-3 Sequence 3 100.0 694 2 US-08-537-400-15 Sequence 1	100.0 694 2 US-08-706-702-17 Sequence 1 100.0 694 3 US-08-706-706-17 Sequence 1	100.0 694 4 US-09-238-4/1-1/ Sequence 1 100.0 696 3 US-09-461-697-193 Sequence 1	100.0 699 3 US-US-461-69/-191 Sequence 1 100.0 705 4 US-09-107-532A-2425 Sequence 2	100.0 711 4 US-09-662-250A-13 Sequence 1 100.0 714 4 US-09-107-532A-3372 Sequence 3	100.0 717 3 US-09-461-697-189 Sequence 18	100.0 720 1 US-08-153-848-35 Sequence 35	100.0 720 2 US-08-722-349-4 sequence 4, 100.0 720 3 US-09-204-328-4 Sequence 4,	100.0 720 3 US-09-299-843A-35 Sequence 3:	100.0 720 4 US-09-107-532A-3104 Sequence 3. 100.0 720 5 US-09-11153-35 Sequence 3. 100.0 723 2 US-08-680-395-2 Sequence 2.

Sequence 1192, Apple Sequence 10. Apple Sequence 2, Appli Sequence 2, Appli Sequence 19, Appli Sequence 26, Appli Sequence 26, Appli Sequence 26, Appli Sequence 27, Appli Sequence 3, Appli Sequence 100, Apple Sequence 15, Appli Sequence 15, Appli Sequence 3, Appli Sequence 169, Appli Seque	
4-001C-1192 6-316-11 0-565-2 9-584-2 9-584-2 9-584-2 9-584-2 9-584-2 8-151A-19 8-151A-23 8-152A-169 8-152A-169 8-189-13 1-1789A-169 8-189-13 1-1789A-169 8-352-2488 8-352-2488 8-352-2488 8-352-2488 8-352-2488 8-352-2488 8-352-2488 8-352-2488 8-352-2488 9-198-169 9-19	
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Sequence 4, Appli Sequence 2968, Appli Sequence 2968, Appli Sequence 118, App Sequence 118, App Sequence 118, App Sequence 118, App Sequence 2, Appli Sequence 2, Appli Sequence 16, Appli Sequence 178, Appli Sequence 178, Appli Sequence 178, Appli Sequence 273, Appli Sequence 273, Appli Sequence 273, Appli Sequence 273, Appli Sequence 274, Appli Sequence 273, Appli Sequence 273, Appli Sequence 273, Appli Sequence 274, Appli Sequence 275, Appli Sequence 276, Appli Sequence 277, Appli Sequence 277, Appli Sequence 278, Appli Sequence	16
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Length 12; 0; Indels

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GENERAL INC. 302/101.

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
COMPETITE OF INVENTION: COMPETITOR PRIMER ASYMMETRIC
TITLE OF INVENTION: POLYMERASE CHAIN REACTION
NUMBER OF SEQUENCES:
COMPESSEE: US. ARMY
ADDRESSEE: US. ARMY
COMPESSEE: US. ARMY
ADDRESSEE: OFFICE OF THE CHER COUNSEL (AMSCB-GC)
CITY: ABERDEEN PROVING GROUND
STREET: OFFICE OF THE CHIEF COUNSEL (AMSCB-GC)
CITY: ABERDEEN PROVING GROUND
STATE: MARYLAND
COUNTRY: USA
ZIP: 21010-5423
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
FILING FILING DATE:
FILING FILING DATE:
FILING FILING FILING DATE:
FILING FILIN
                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: third strand derived from M. luteus
DESCRIPTION: 23s region in Seq ID No. 5861244245
                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: no
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 246 :FROM 1 TO
US-08-173-489C-246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.0%; Score 10; DB 2;
Matches 10; Conservative 0; Mimmaral
TELECOMMUNICATION INFORMATION:
TELEPHONE: (attorney) (212) 708-1880
TELEFAX: (attorney) (212) 246-8959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DAM 398-94
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NAME: BIFFONI, ULYSSES J
REGISTRATION NUMBER: 39,908
REFERENCE/DOCKET NUMBER: DAM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 410-671.1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 3, Application US/08628417
; Patent No. 5627054
                                                                                         INFORMATION FOR SEQ ID NO: 246:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 bases
TYPE: nucleic acid
STRANDEDNESS: single stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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ORIGINAL SOURCE:
ORGANISM: Sta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL:
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100.0%; Pred. No. 2e+03;
tive 0; Mismatches 0; Indels
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APPLICANT: WANG, C. -G.
APPLICANT: HEBURN, A. G.
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Hepatitis B virus
INDIVIDUAL ISOLATE: adw2
INDIVIDUAL ISOLATE: adw2
PUBLICATION INFORMATION:
AUTHORS: Valenzuela, P., Quiroga, M, Zaldivar, J,
AUTHORS: Gray, P., Ruter, W J.
TITLE: The nucleotide sequence of
TITLE: the Hepatitis B viral genome and the
TITLE: identification of the major viral genes
JOURNAL: In "Animal Virus Genetics", Fields, B N,
JOURNAL: Jaenisch, R, FOX C F eds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVESTION: INTELESTICAL CONTRESS:
CORRESPONDENCES: 365
CORRESPONDENCES: 365
CORRESPONDENCES: PROFILE DIAGNOSTIC SCIENCES, INC., STREET; 510 BAST 73RD STREET,
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10021.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 25 DEC 1993
CLASSIFICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, JOSEPH H.
REFERENCE/DOCKET NUMBER: 26,179
REFERENCE/DOCKET NUMBER: 26,179
                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: genomic DNA DESCRIPTION: hepatitis B virus adw2 isolate, DESCRIPTION: nucleotides 807 to 818
                             y) (212) 708-1880
(212) 246-8959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 2
US-08-173-489C-246
'S-Sequence 246, Application US/08173489C
'Patent No. 5861244
             TELECOMMUNICATION INFORMATION:
TELEPHONE: (attorney) (212) 708-
TELEFAX: (attorney) (212) 246-89
INFORMATION FOR SEQ ID NO: 181:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: mucleic acid
STRANDEDNESS: double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Conservative
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Best Local Similarity
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-173-489C-181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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US-09-198-484-8/C
j Sequence 8, Application US/09198484
j Patent No. 6162435
j GENERAL INFORMATION:
j APPLICANT: Milion, F. Chris
j APPLICANT: Milion, F. Chris
j TILE OF INVENTION: RECOMBINANT MYCOPLASMA HYDPNEUMONIAE VACCINE
j FILE REFERENCE: 1900.028/P028
j CURRENT FILING DATE: 1998-11-24
j NUMBER OF SEQ ID NOS: 10
j SEQ ID NO 8: 10
j SEQ ID NO 8: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
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| Sequence 65, Application US/08173489C|
| Patent No. 5861244|
| Patent No. 586124|
| Patent No. 58614|
| Patent N
                                                                                                                                                                                                                                                                                                                                       Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 10; DB 3; I
100.0%; Pred. No. 1.9e+03;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 10; DB 2; I
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 10; Conservative 0; Mismatches 0;
TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Other nucleic acid;

DESCRIPTION: Synthetic DNA oligonucleotide

US-08-229-528-16
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MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: 18M FC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 2.2 DEC 1993
CLASSIFICATION: 435
RIOR APPLICATION DATA:
RAPPLICATION DATA:
RAPPLICATION UNBER: US 07/968,436
FILING DATE: 29 OCT 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 CTTCTCTTT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
CRGANISM: primer
US-09-198-484-8
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US-09-108-452A-6382/C
US-09-108-452A-6382/C
Sequence 6582, Application US/09198452A
Sequence 6582, Application US/09198452A
Sequence 6582, Application US/09198452A
GENERAL INFORMATION:
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever TITLE OF INVENTION: and treatment of infection
TITLE OF INVENTION: and treatment of infection
FILE REPRENEUR: 971-003-999
CURRENT PEDLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 6382
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
US-08-229-528-16/C
Sequence 16, Application US/08229528
Sequence 16, Application US/08229528
Sequence 10, Application US/08229528
SEQUENCE 10, ADDRESS:
TITLE OF INVENTION:
NUMBER OF ENVENTION:
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESS:
ADDRESS:
ADDRESS:
ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
AD
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                                                        100.0%; Score 10; DB 1; Length 20; 100.0%; Pred. No. 1.9e+03; tive 0; Mismatches 0; Indels
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STATE: Wisconsin
COUNTRY: Wisconsin
COUNTRY: USA
ZIP: 5370-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM FC compatible
OPERATING SYSTEM: MS-DOS 3.3
SOFTWARE: WordPerfect, Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/229,528
FILING DATE: 18-APR-1994
PRIOR APPLICATION NUMBER: 07/868,569
FILING DATE: 15-APR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30383/133
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REGISTRATION NUMBER: 30,136
REFERENCE/DOCKET NUMBER: 30383
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 258-4284
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 base pairs
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Best Local Similarity 100.
Matches 10; Conservative
                                                                                                             Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                           8 CTTCTCTTTT 17
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                                                                          Query Match
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MOLECULE TYPE: Other nucleic acid
MOLECULE TYPE: Vb region)
HYPOTHETICAL: No
ORIGINAL SOURCE: Synthesized using
ORIGINAL SOURCE: Oligonucleotide synthesis machine
PUBLICATION INFORMATION:
AUTHORS: Alessandra; Bettinardi, Alessandra; Puoti, Massimo; Primi,
AUTHORS: Daniele
TITLE: Selective Depletion in HIV Infection
TITLE: of T Cells That Bear Specific T Cell Receptor Vb Sequences
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Sequence 17, Application US/08320336

Sequence 17, Application US/08320336

Patent No. 58935623

GENERAL INFORMATION:
TITLE OF INVENTION: Diagnosis and Treatment of TITLE OF INVENTION: AIDS Onset
NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:
ADDRESSEE: Thomas E. Popovich, Thomas
ADDRESSEE: Popovich & Associates
STREET: 80 South 8th Street
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISSUE: 5033
PAGES: 860-862
PUBLICATION DATE: No. 5665355ember 8, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 55402-2111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible Compaq Prolinea
COMPUTER: 4/66
APPLICATION NUMBER: 07/973,485
FILING DATE: No. 566535ember 9, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. POPOVICH
REGISTRATION NUMBER: 3678
TELEPHONE: (612) 334-8991
TELEPHONE: (612) 334-8991
TELEPHONE: (612) 334-8994
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTAR: 1/09
COMPUTAR: 1/09
COMPUTARE: Microsoft Word for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/320,306
FILING DATE: 06-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                       LENGTH: 24 bases
TYPE: Nucleic Acid
STRANDEDNESS: Single
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254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-488-212A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOWE:
CHROMOSOME/SEGMENT: chromosome 2
MAP POSITION: 2q33-q35
PUBLICATION Seakin, S O, Breitman, M L, Tsui, L C.
TITLE: Structural and evolutionary
TITLE: relationships among five members of the human
TITLE: gamma-crystallin gene family
JONRAAL: Molecular and Cellular Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 10; DB 2; Length 22
100.0%; Pred. No. 1.9e+03;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: Genomic DNA
DESCRIPTION: gamma-crystallin gene exon 3
DESCRIPTION: (Accession # K03006) nucleotides 9 to 30
HYPOTHETICAL: No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DATE: 1985
RELEVANT RESIDUES IN SEQ ID NO: 65 :FROM 1 TO 22
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US-08-488-212A-17/c

Sequence 17, Application US/08488212A

PETERT NO. 5665355

GENERAL INFORMATION:
APPLICANT: Primi, Daniele
TITLE OF INVENTION: Diagnosis and Treatment of
TITLE OF INVENTION: Diagnosis and Treatment of
TITLE OF INVENTION: Diagnosis and Treatment of
TITLE OF INVENTION: Daniele
TITLE OF INVENTION: Daniele
AUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:
ADDRESSEE: Popovich & Associates
ADDRESSEE: Popovich & Associates
STREET: Minneapolis
STREET: Minneapolis
STATE: Minneapolis
STATE: Minneapolis
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 55402-2111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
MEDIUM TYPE: Storage
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                                                     NAME: Handelman, Joseph H.

REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: 05189
RELECOMUNICATION INFORMATION:
TELEPAN: (attorney) (212) 708-1880
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
ITYPE: Nucleic Acid
STRANDEDNESS: duble stranded
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: MS-DOS Version 5
SOFTWARE: Microsoft Word for Windows
CURRENT APPLICATION DATA:
FILING DATE: 07-Jun-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                               ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Best Local Similarity
Matches 10; Conserv
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Query Match
Best Local Similarity 100.0
Matches 10; Conservative
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TYPE: Nucleic Acid
STRANDEDNESS: Single
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860-862
                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL: NO ORIGINAL SOURCE: ORIGINAL SOURCE:
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US-08-408-011-17/c
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                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: Other nucleic acid MOLECULE TYPE: Other nucleic acid MOLECULE TYPE: (oligonucleotide useful in amplification of T Cell Receptor MOLECULE TYPE: Vb region)
HYPOTHERICAL: No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS: Imberti, Luisa, Sottini,
AUTHORS: Alessandra, Bettinardi, Alessandra; Puoti, Massimo; Primi,
AUTHORS: Daniele
TITLE: Selective Depletion in HIV Infection
TITLE: of T Cells That Bear Specific T Cell Receptor Vb Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 10; DB 2; Length 24; 100.0%; Pred. No. 1.9e+03; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE: Synthesized using ORIGINAL SOURCE: oligonucleotide synthesis machine PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17, Application US/08488209B
Patent No. 5925513
GENERAL INFORMATION:
APPLICANT: Primi, Daniele
TITLE OF INVENTION: Diagnosis and Treatment of
TITLE OF INVENTION: AIDS Onset
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thomas E. Popovich, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISSUE: 5033
PAGES: 860-862
PUBLICATION DATE: No. 5891623ember 8, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 55402-2111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible Compag Prolinea
COMPUTER: 4/66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: MS-DOS Version 5
SOFTWARE: Microsoft Word for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,209B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
RELING DATE: NO. 5925513ember 9, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Thomas E. Popovich, Thomas ADDRESSEE: Popovich & Associates STREET: 80 South 8th Street (ITY: Minneapolis STATE: Minnesota
FILING DATE: No. 5891623ember 9, 1992 ATTORNEY/AGENT INFORMATION:
                                      NAME: Thomas E. Popovich
REGISTRATION NUMBER: 30099
REFERENCE/DOCKET NUMBER: 3678
TELECOMMUNICATION INFORMATION:
TELEPAN: (612) 334-8991
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.(
Matches 10; Conservative
                                                                                                                                                                                                                        LENGTH: 24 bases
TYPE: Nucleic Acid
STRANDEDNESS: Single
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                                                                                                                                                                                                                                                                                                Linear
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US-08-488-209B-17/c
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ATTORNEY/AGENT TROOMATION:

AND THORNEY/AGENT TROOMATION:

RESISTRATION WINDERS: 30099

RESIDENCE TOWER WI
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100.0%; Score 10; DB 6; Length 24; 100.0%; Pred. No. 1.9e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                      Score 10; DB 3; Length 24; Pred. No. 1.9e+03; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 24;
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;Patent No. 5336598
; APPLICANT: KOZZIN, BRIAN L.;MARRACK, PHILIPPA;KAPPLER,
;JOHN,CHOI, YOUNGWON
; TITLE OF INVENTION: METHOD FOR DIAGNOSING A SUPERANTIGEN
;CAUSED PATHOLOGIAL CONDITION VIA ASSAY OF T-CELLS
; UUMBER OF SEQUENCES: 25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/437,370
; FILING DATE: 15-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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llarity 100.0%; Pred. No. 1.9e+03;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09417722 Patent No. 6309837
                                                                                                                                                                                                                           100.0%;
100.0%;
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Best Local Similarity 100.4
Matches 10, Conservative
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                 LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CTICTCTITI 10
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                                                                                                                                         linear
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Matches 10, Conserv
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US-08-559-205-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-417-722-3/c
                                                                                                                                         TOPOLOGY:
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                                                                                                                                                                                                                                                                       MOLECULE TYPE: Other nucleic acid
MOLECULE TYPE: Other nucleic acid
MOLECULE TYPE: (oligonucleotide useful in amplification of T Cell Receptor
MOLECULE TYPE: Wb region)
HYPOTHETICAL: No
ORIGINAL SOURCE: Synthesized using
ORIGINAL SOURCE: oligonucleotide synthesis machine
PUBLICATION INFORMATION:
AUTHORS: Imberti, Luisa; Sottini,
AUTHORS: Imberti, Luisa; Sottini,
AUTHORS: Daniele
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APPLICANT: Liu, Debang
APPLICANT: Liu, Debang
TITLE OF INVENTION: Cell Receptor ' and Chain CDR3 Regions
TITLE OF INVENTION: Cell Receptor ' and Chain CDR3 Regions
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE: Selective Depletion in HIV Infection
TITLE: of T Cells That Bear Specific T Cell Receptor Vb Sequences
VOLUME: Science
VOLUME: 254
ISSUE: 5033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/559,205
FILING DATE:
CLASSIFICATION: 436
ATTONREY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/POCKET UNBER: 28721/32972
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 10; DB 2; L 100.0%; Pred. No. 1.9e+03; cive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISSUE: 5033
PAGES: 860-862
PUBLICATION DATE: No. 5928642ember 8, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 6300 Sears Tower, 233 Sout CITY: Chicago STATE: 111inois COUNTRY: United States of America ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16, Application US/08559205
Patent No. 6087096
GENERAL INFORMATION:
                         REGISTRATION NUMBER: 30099
REFERENCE/DOCKET UNMBER: 36
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 334-8991
                                                                                                                  TELEFAX: (612) 334-8994
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
         Thomas E. Popovich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                            ULENGTH: 24 bases
TYPE: Nucleic Acid
empanDEDNESS: Single
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US-08-559-205-16/c
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  Gaps
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US-09-417-722-3
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APPLICANT: Bean; Yi-Hong
TITLE OF INVENTION: PCR-based Method for Identifying a Fusarium
TITLE OF INVENTION: PCR-based Method for Identifying a Fusarium
TITLE OF INVENTION: Wilt-Resistant Genotype in Plants
FILE REFERENCE: PCR ID: Fusarium-resistant genotype
CURRENT APPLICATION NUMBER: US/09/417,722
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NOS: 4
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US-08-412-376-23/c

Sequence 23, Application US/08412376

GENERAL INFORMATION:
TITLE OF INVENTION: Inhibition Of Viruses By Antisense
TITLE OF INVENTION: Stranded RNA Or RNA-DNA Hybrids
NUMBER OF SEQUENCES:
NUMBER OF SEQUENCES:
ADDRESSEE: Woodcock Washburn Kurtz
ADDRESSEE: Macdiewicz & No. 5849900ris
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: 1BM PS/2
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 10; DB 2; I
100.0%; Pred. No. 1.9e+03;
Live 0; Mismatches 0;
       100.0%; Score 10; DB 6; I
100.0%; Pred. No. 1.9e+03;
                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPLIANT LAW FOX.

COMPLIANT LAW FOX.

SOFTWARE: WORDFERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/412,376

FILING DATE: Herewith

CLASSIFFCATION: 514

RAPLICATION SATA:

APPLICATION NUMBER: US 07/954,184

PRIOR APPLICATION INTORNATION:

NAME: DOLEGN YAKE TRUJILO

REGISTRATION NUMBER: 35,719

REPERBUCE/DOCKET NUMBER: APPL-0021

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3130

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE: CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 18
US-08-584-040-7049/C
US-08-584-040-7049, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
; APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APOL-0021
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Best Local Similarity 100.
Matches 10; Conservative
                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: Nucleic Acid
STRANDEDNESS: Single
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                                                                                                                                                13 CITCICITIT 4
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Ouery Match
Best Local Similarity
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5217891-9(c
5217891-9(c
5217891-9(c
7) Patent No. 5217891
7 TITLE OF INVENTION: DNA CONSTRUCTS CONTAINING A KLUYVEROMYCES
7 ATTER OF INVENTION: FOR DIRECTING SECRETION OF HETEROLOGOUS
POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%; Score 10; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 21010-5423
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: The PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
SOFTWARE: PATENTIN DATA: US/08/628,417
APPLICATION NUMBER: US/08/628,417
FILING DATE:
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: BIFFONI, ULYSEES J
REFERENCE/DOCKET NUMBER: DAM 398-94
REFERENCE/DOCKET NUMBER: DAM 398-94
TELECOMMUNICATION INFORMATION:
TELEPANIC: 410-671-2534
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 bases
LENGTH: 25 bases
                                                                                           Sequence 4, Application US/08628417;
Sequence 4, Application US/08628417;
Patent No. 5627054
GENERAL INFORMATION:
APPLICANT: GILLESPIE, DAVID
TITLE OF INVENTION: COMPETITOR PRIMER ASYMMETRIC
TITLE OF INVENTION: POLYMERASE CHAIN REACTION
NUMBER OF SEQUENCES:
ADDRESSEE: U.S. ARMY CHEMICAL AND BIOLOGICAL
ADDRESSEE: U.S. ARMY CHEMICAL AND BIOLOGICAL
ADDRESSEE: DEFENSE COMMAND
STREET: OFFICE OF THE CHIEF COUNSEL (AMSCB-GC)
CITY: ABERDEEN PROVING GROUND
STREET: MARYLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 23
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/507,398
FILING DATE: 09-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 78,551
FILING DATE: 28-JUL-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: oligodeoxynucleotide
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STRANDEDNESS: single
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US-08-628-417-4
                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                           US-08-628-417-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5217891-9
                                                                        RESULT 15
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Gaps

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US-09-270-542-132
; Sequence 132.
Patent No. 6322976
; GENERAL INFORMATION:
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CRGANISM: Rattus norvegicus
US-09-270-542-134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Rattus norvegicus
US-09-270-542-132
                                                                                               , ORGANISM: Rattus norvegicus US-09-270-542-133
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Best Local Similarity 100.
Matches 10; Conservative
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LENGTH: 29
TYPE: DNA
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Sequence 133, Application US/09270542

Sequence 133, Application US/09270542

GENERAL INFORMATION:

APPLICANT: Altman, Timothy

APPLICANT: Stanton, Lawrence

TITLE OF INVENTION: Compositions and Methods of Disease Diagnosis and

TITLE OF INVENTION: Compositions and Methods of Disease Diagnosis and

TITLE OF INVENTION: Therapy

TITLE OF INVENTION Therapy

CURRENT APPLICATION NUMBER: US/09/270,542

CURRENT APPLICATION NUMBER: 09/221,222

BARLIER APPLICATION NUMBER: 09/221,222

ADMISSION NUMBER: 09/221,222

ADMISSION NUMBER: 09/221,222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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     METHOD AND REAGENT FOR THE TREATMENT OF DISEASES OR CONDITIONS RELATED TO LEVELS OF VASCULAR ENDOTHELIAL GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                    COUNTER: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700 CITY: Los Angeles STREET: California COUNTEY: U.S.A.

ZIP: 90071-2066
COMPUTER: BEADABLE FORM: WEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: Storage COMPUTER: EM COMPATIBLE STORAGE COMPUTER: BM COMPATIBLE STORAGE SOFTWARE: WORD PEFFECT 5.1 CURRENT APPLICATION DATA: APPLICATION DAT
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                      TITLE OF INVENTION: TREE
TITLE OF INVENTION: CONI
TITLE OF INVENTION: CF INTLE OF INVENTION: CRO
NUMBER OF SEQUENCES: 85C
CORRESPONDENCE ADDRESS:
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| Sequence 134, Application US/09270542
| Sequence 134, Application US/09270542
| Patent No. 6322970
| GENERAL INFORMATION:
| APPLICANT: Aitman, Timothy
| APPLICANT: Scott, James
| TITLE OF INVENTION: Compositions and Methods of Disease Diagnosis and
| TITLE OF INVENTION: Therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Strain, Timothy
APPLICANT: Strain, Timothy
APPLICANT: Strain, James
APPLICANT: Strain, James
APPLICANT: Strain, James
APPLICANT: Strain, Jawrence
TITLE OF INVENTION: Compositions and Methods of Disease Diagnosis and
TITLE OF INVENTION: Therapy
FILE REFERENCE: 4198/78179
FILE REFERENCE: 4198/78179
CURRENT APPLICATION NUMBER: US/02/203-17
EARLIER APPLICATION NUMBER: 09/221,222
RALIER FILING DATE: 1999-12-23
NUMBER: OF SEQ ID NOS: 207
SCPTWARE: Patentin Ver. 2.0
SEQ ID NO 132
                                                                                                                              Gaps
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100.0%; Score 10; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 10; Conservative 0; Mismatches 0; Indels
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Query Match
100.0%; Score 10; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 10; Conservative 0; Mismatches 0; Indels
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                                                                                                                            Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                  0; Indels
                                                                                                                            100.0%; Score 10; DB 3; I
100.0%; Pred. No. 1 9e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/536,784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PILLING DATE: 30-Oct-1997
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
ATTORNEY/AGBNT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPERENCE/DOCKET NUMBER: P8340P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 359:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; SEQUENCE DESCRIPTION: SEQ ID NO: 359: US-09-536-784-359
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US-09-371-772B-10906/c
; Sequence 10906, Application US/09371772B
; Parent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-083-359
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                                                                                                                                     Sequence 135, Application US/09270542

Sequence 135, Application US/09270542

Patent No. 6322976

GENERAL INFORMATION:

APPLICANT: Aitman, Timothy

APPLICANT: Scott, James

TITLE OF INVENTION: Compositions and Methods of Disease Diagnosis and

TITLE OF INVENTION: Therapy

TITLE OF INVENTION: Therapy

FILE REPRENCE: 4198/78179

CURRENT FILING DATE: 1999-03-17

EARLIER APPLICATION NUMBER: 09/221,222

EARLIER PILING DATE: 1999-12-23

NUMBER OF SEQ ID NOS: 207

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 135

LENGTH: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 359, Application US/08961083
Patent No. 6159469
GENERAL INFORMATION:
APPLICANT: Choi et al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Huan Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STRIEE: Maryland
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ZIP: 20850

MODIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII TEXT

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/961,083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 10; DB 4; I ilarity 100.0%; Pred. No. 1.9e+03; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INPORMATION:
TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 359:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Rattus norvegicus US-09-270-542-135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CTTCTCTTTT 10
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        CTICICITII 10
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Best Local Similarity
Matches 10; Conserv
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                                                                                                           RESULT 22
US-09-270-542-135
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                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                             ) OTHER INFORMATION: Description of Artificial Sequence:PCR-G-FOR (p53 ) OTHER INFORMATION: Exon 8) US-09-277-016-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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APPLICANT: FISHER, CHARLES W.
APPLICANT: BARNES, HENRY J.
APPLICANT: ESTABROOK, RONALD W.
APPLICANT: ESTABROOK, RONALD W.
TITLE OF INVENTION: THE EXPRESSION OF BILOGICALLY
TITLE OF INVENTION: ACTIVE FUSION PROTEINS COMPRISING A
TITLE OF INVENTION: ACTIVE FUSION PROTEINS COMPRISING A
TITLE OF INVENTION: ACTIVE FUSION PROTEINS COMPRISING
TITLE OF INVENTION: A REDUCTASE IN BACTERIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DURKEE
STREET: P.O. BOX 4433
CONTY: HOUSTON
CONTY: HOUSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 10; DB 1; Length 42; 100.0%; Pred. No. 1.9e+03; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                              100.0%; Score 10; DB 3; Length 40; 100.0%; Pred. No. 1.9e+03;
                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
COMPUTER: BW PC COMPATIBLE
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/908,317
EARLIER APPLICATION NUMBER: 08/700,583
EARLIER FILING DATE: 1996-08-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20
LENGTH: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 33, Application US/07908317
Patent No. 5420027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32,165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 19920702
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, DAVID L
REGISTRATION NUMBER: 32,16:
REFRENCE/DOCKET NUMBER: UT
                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELERAX: 512-474-7577
TELEX: NOT APPLICABLE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Matches 10; Conservative
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 10; Conservative
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TYPE: NUCLEIC ACID
STRANDEDNESS: single
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US-07-908-317-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 28
US-07-908-317-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
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                                                                                                                                                                                              FEATURE:
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APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchoomb, Dan
APPLICANT: Stinchoomb, Dan
APPLICANT: Stinchoomb, Dan
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascalar Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vascalar Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vascalar Endothelial Growth Factor Receptor
CURRENT FILING DATE: 1995-08-10
FRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patentin version 3.0
SEQ ID NO 10906
LENGTH: 38
THENGTH: 38
THENGTH: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-10906
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Sequence 20, Application US/09277016
Sequence 20, Application US/09277016
Sequence 20, Application US/09277016
Sequence 20, Application US/09277016
Sequence 20, No. 6143529
FIGURATION: Bellow Stanley N
APPLICANT: Shuber, Anthony P
FILE OF INVENTION: Screening assays
FILE REFERENCE: EXT-030
CURRENT FILING DATE: 1999-03-26
SEARLIER APPLICATION NUMBER: 08/09/277,016
SEARLIER APPLICATION NUMBER: 08/09/277,016
SEARLIER APPLICATION NUMBER: 08/09/277,016
SEARLIER APPLICATION NUMBER: 08/09/277,016
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;Patent No. 5217891
ANTHONY J.;VAN DEN BERG, JOHAN A.
TITLE OF INVENTION: DNA CONSTRUCTS CONTAINING A KLUYVEROMYCES;
A FACTOR LEADER SEQUENCE FOR DIRECTING SECRETION OF HETEROLOGOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 10; DB 6; Length 39; 100.0%; Pred. No. 1.9e+03;
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100.0%; Pred. No. 1.9e+03;
:ive 0; Mismatches 0;
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(URRENT APPLICATION DATA:

CURRIT APPLICATION NUMBER: US/08/507,398

FILING DATE: 09-APR-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 78,551

FILING DATE: 28-JUL-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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LENGTH: 39
5217891-13
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Sequence 765, Application US/09671317

Sequence 765, Application US/09671317

Patent NO. 6528260

GENERAL INFORMATION:
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
APPLICANT: Chen, Annick
TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
TITLE OF INVENTION BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
TITLE REFERENCE: 62.U33.CIP
CURRENT FILING DATE: 2000-09-27
CURRENT PELING DATE: 2000-09-27
FRIOR APPLICATION NUMBER: US 60/136,269
FRIOR FILING DATE: 2000-03-24
FRIOR FILING DATE: 1999-03-25
FRIOR FILING DATE: 1999-03-25
FRIOR PILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 977
SROW APPLICATION NUMBER: US 60/131,961
FRIOR PILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 977
SROW APPLICATION NUMBER: US 60/131,961
FRIOR PILING DATE: Patent.pm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 5258302
; Patent No. 5258302
; Patent No. 5258302
; Patent No. 5258302
; MAYS S. PROCKHOLZ, THOMAS S.; ENGEL, MICHAEL E.; URCAN,
; MATTLE OF INVENTION: DNA FOR EXPRESSION OF APROTININ IN
; METHALOTROPHIC YEAST CELLS
; NUMBER OF SEQUENCES: 31
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/560,618
; FILING DATE: 30-UUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 547,985
; FILING DATE: 03-UUL-1990
; FILING DATE: 03-UUL-1990
                                                                                                                                                                                                                                        100.0%; Score 10; DB 5; Length 42; 100.0%; Pred. No. 1.9e+03; Live 0; Mismatches 0; Indels
TELBFAX: S12-474-7577

TELEX: NOT APPLICABLE

INFORMATION FOR SEQ ID NO: 3

SEQUENCE CHARACTERISTICS:

LENGTH: 42 base pairs

TYPE: nucleic acid

TYPE: nucleic acid

TYPE: TOPOLOGY: linear

TOPOLOGY: linear
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Best Local Similarity 100.
....hes 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO:15:
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                                                                                                                                                                                                            APPLICANT: LOGENT NEUROSCIENCE, Inc.
APPLICANT: Lo, Donald C.
APPLICANT: Thomas, Mary Beth
APPLICANT: Thomas, Mary Beth
APPLICANT: Puranam, Kasturi
APPLICANT: Puranam, Kasturi
APPLICANT: Puranam, Kasturi
APPLICANT: Puranam, Kasturi
APPLICANT: Puranam, ComPositions and METHODS FOR DIAGNOSING
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DISBASES INVOLVING
TITLE OF INVENTION: CELL DEATH
FILLE REFERENCE: 10001-005-999
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOUTHARE: FastSEQ for Windows Version 4.0
SEQ ID NO 227
LENGTH: 42
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100.0%; Score 10; DB 3; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 10; Conservative 0; Mismatches 0; Indels
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TITLE OF INVENTION: BUKARYOTIC CYTOCHROME P450 FUSED TO
TITLE OF INVENTION: A REDUCTASE
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSE: ARNOLD, WHITE & DURKEE
STREET: P.O. BOX 4433
CITY: HOUSTON
STATE: TEXAS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTSD:292/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-320-7200
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COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06171
FILING DATE: 19930629
CLASSIFFCATION:
PRIOR APPLICATION:
PRIOR APPLICATION OBTA:
APPLICATION NUMBER: 07/908,317
FILING DATE: 02 July 1992
ATTORNEY/AGENT INFORMATION:
NAMME: PARKER, DAVID L.
REGISTRATION NUMBER: 32,1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT-US93-06171-33
; Sequence 33, Application PC/TUS9306171
; Sequence In Application:
    APPLICANT:
                                                                                                                                                  Sequence 227, Application US/09461697
Patent No. 6277974
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CTICICITII 10
          ; TYPE: DNA; CORGANISM: Homo sapiens
US-09-461-697-227
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GENERAL INFORMATION:

APPLICANT: Colon, Daniel
APPLICANT: Colon, Daniel
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET .020CP1
CURRENT APPLICATION NUMBER: US 09/298,850
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER PLING DATE: 1999-04-21
EARLIER PLING DATE: 1998-11-23
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 1546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cohen, Daniel
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfield, Marta
APPLICANT: Blumenfield, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REPERBNCE: GENSET. 020cPl
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT APPLICATION NUMBER: US 09/298,850
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1999-04-21
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: US 60/082,614
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LENGTH: 47

TYPE: DNA

CORGANISM: Homo Sapiens

FRATURE:

NAME/KEY: allele

LOCATION: 24

GOTHER INFORMATION: 99-22604-208 : polymorphic base G or T
US-09-422-978-1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: 99-4541-39 : polymorphic base G or T
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llarity 100.0%; Pred. No. 1.9e+03;
Conservative 0; Mismatches 0;
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; Patent No. 6537751
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1546, Application US/09422978
Patent No. 6537751
                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                               13 CTTCTTTT
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Best Local Similarity
Matches 10; Conserv
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APPLICANT: Cohen, Daniel

APPLICANT: Chunakov, 11ya

APPLICANT: Blumenfeld, Marta

APPLICANT: Blumenfeld, Marta

APPLICANT: Blumenfeld, Marta

APPLICANT: Chunakov, 11ya

TITE OF INVENTION: Biallelic markers for use in constructing a high density...

FILE REFERENCE: GENSET.020CP1

CURRENT APPLICATION NUMBER: US 09/298,850

EARLIER APPLICATION NUMBER: US 60/109,732

EARLIER PLILNG DATE: 1998-11-23

EARLIER PLILNG DATE: 1998-11-23

EARLIER PLILNG DATE: 1998-11-33

EARLIER PLILNG DATE: 1998-11-34

EARLIER PLILNG DATE: 1998-04-21

MUMBER OF SEQ ID NOS: 11796

SEQ ID NO 1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cohen, Daniel
APPLICANT: Cohen, Daniel
APPLICANT: Chumenfeld, Marta
APPLICANT: Chumenfeld, Marta
APPLICANT: Chumenkev, 11
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-04-21
BARLIER FILING DATE: 1999-04-21
BARLIER FILING DATE: 1998-11-23
BARLIER FILING DATE: 1998-11-23
BARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NOS: 11796
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                                                                                                                                         100.0%; Score 10; DB 4; Length 47; 100.0%; Pred. No. 1.9e+03; 1ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: allele
LOCATION: 24
CHER INFORMATION: 99-15101-154 : polymorphic base G or C
08-09-422-978-52
                                 NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: 12-602-196 : polymorphic base C or T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 34
2.09-422-978-1282
; Sequence 1282, Application US/09422978
; Patent No. 6537751.
                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 522, Application US/09422978; Patent No. 6537751; GENERAL INFORMATION:
                                                                                                                                                                         Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CTTCTCTTTT 10
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ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                 RESULT 33
US-09-422-978-522/c
                                                              ; LOCATION: 24
; OTHER INFORMAT
US-09-671-317-765
                                                                                                                                                      Query Match
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; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/461,697
; CURRENT FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 225
LENGTH: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: BAKER & BOTTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Conservative
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                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CTTCTCTTTT 10
                                                                                                                                                                                                                                                                                                                                                                 1 CTTCTCTTT 10
                                                                                                                                                                                                                                                                                                                                                                                                          20 Crrcrcrrrr 11
                                                                                                                                                                                   TYPE: DNA
CRGANISM: Homo sapiens
US-09-461-697-225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: CDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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US-08-910-632-40/c
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GENERAL GENSET.020CP1
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER FILING DATE: 1999-10-20
EARLIER FILING DATE: 1999-10-20
EARLIER FILING DATE: 1999-10-20
EARLIER FILING DATE: 1999-10-21
EARLIER FILING DATE: 1998-10-21
EARLIER FILING DATE: 1998-10-23
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-10-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 3284
LENTHH: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: Example C.
APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart D.
APPLICANT: Puranam, Kasturi
APPLICANT: Ratz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
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                                                                                                                                                                                                                                                                                   Length 47;
                                                                                                                                                                                                                                                                                 100.0%; Score 10; DB 4; Length 47 100.0%; Pred. No. 1.9e+03; tive 0; Mismatches 0; Indels
                                                                                                                                                              NAME/KEY: allele

LOCATION: 24

COTHER INFORMATION: 99-11191-86 : polymorphic base A or G

US-09-422-978-2472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: 24
; OTHER INFORMATION: 99-2981-53 : polymorphic base T or C
US-09-422-978-3284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-422-978-3284/c
; Sequence 3284, Application US/09422978
; Patent No. 6537751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-461-697-225/c
; Sequence 225, Application US/09461697
; Patent No. 6277974
                  EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 2472
LENGTH: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo Sapiens
                                                                                                              TYPE: DNA ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: allele
                                                                                                                                                         FEATURE:
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105-08-477-928A-37/c

15 Sequence 37, Application US/08477928A

17 SEQUENCE 37, Application US/08477928A

18 SEQUENCE 37, Application US/08477928A

18 SEQUENCE 37, Application US/08477928A

18 SEQUENCE 38 SEQUENCE 38

18 TILE OF INVENTION: LYMPHOCYTE MEDIATED IMMUNE RESPONSES

19 CORRESPONDENCE ADDRESS:
100.0%; Score 10; DB 3; Length 48; 100.0%; Pred. No. 1.9e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: BACKER & DOILS
GTREET: 1299 Pennsylvania Avenue
CTTY: Washington D.C.
STATE: California
COUNTRY: U.S.A.
ZIP: 20004-2400
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,928A
FILING DATE: O7-JUN-1995
CLASSIFICATION : 536
ATTORNEY/AGENT INFORMATION:
NAME: REPRENCE/DOCKET NUMBER: 19060-0105
TELEFRANCE/DOCKET NUMBER: 19060-0105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 10; DB 3; I
100.0%; Pred. No. 1.9e+03;
Live 0; Mismatches 0;
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APPLICANT: KOOL, ERIC T.

TITLE OF INVENTION:

FILE REFERENCE: 220.00010130

CURRENT APPLICATION NUMBER: US/08/910,632B

CURRENT APPLICATION NUMBER: US/08/910,632B

CURRENT APPLICATION NUMBER: US/08/910,632B

EARLIER APPLICATION NUMBER: US/08/93,439

EARLIER FILING DATE: 1997-02-23

EARLIER FILING DATE: 1995-02-23

EARLIER FILING DATE: 1995-04-15

MUMBER OF SEQ ID NOS: 83

SOFTWARE: PARLICATION NUMBER: 08/047,860

EARLIER FILING DATE: 1993-04-15

NUMBER OF SEQ ID NOS: 83
                                                                  APPLICANT: KOOL, ERIC T.

TITLE OF INVENTION: HIGHLY SENSITIVE MULTIMERIC NUCLEIC ACID PROBES
FILE REPRENCES: 220.0010130
CURRENT APPLICATION NUMBER: US/08/910,632B
CURRENT FILING DATE: 1997-08-13
FARLIER APPLICATION NUMBER: 08/085,631
EARLIER FILING DATE: 1997-02-26
EARLIER FILING DATE: 1995-02-23
EARLIER FILING DATE: 1995-02-23
EARLIER FILING DATE: 1993-04-15
NUMBER OF SEQ ID NOS: 83
SOFTWARE: PATENTING DATE: 1993-04-15
SOFTWARE: PATENTING DATE: 1993-04-15
SEQ ID NO 40
LENGTH: 53
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CTHER INFORMATION: stem-loop RNA multimer which binds HIV-1 gag RNA

US-08-910-632-41
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100.0%; Score 10; DB 3; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 10; DB 3; Length 53; 30.0%; Pred. No. 1.9e+03; tive 7; Mismatches 0; Indels
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US-08-805-631A-40/c
S.equence 40, Application US/08805631A
Patent No. 6096880
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 41, Application US/08910632B
; Patent No. 6077668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: DNA 53mer circle
Sequence 40, Application US/08910632B
Patent No. 6077668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 30.0°
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                                                    GENERAL INFORMATION:
APPLICANT: KOOL, ER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 41
US-08-910-632-41
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LENGTH: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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| Sequence 41. Application US/08805631A |
| Sequence 41. Application US/08805631A |
| Patent No. 6096880 |
| GENERAL INFORMATION: |
| TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND TITLE OF INVENTION: DNA |
| TITLE OF SEQUENCES: 72 |
| CORRESPONDENCE ADDRESS: 73 |
| ADDRESSE: MUETING, RAASCH & GEBHARDT, P.A. |
| STREET: 119 No. 6096880th Fourth Street, Suite 201 |
| CITY: Minneapolis |
| STATE: Minneapolis |
| COUNTRY: USA
APPLICANT: UNIVERSITY OF ROCHESTER
TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND
TITLE OF INVENTION: DNA
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
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                                                                                                           ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
STREET: 119 No. 6096880th Fourth Street, Suite 201
CITY: Minneapolis
STATE: Minnesota
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/805,631A
FILING DATE: 26-FEB-97
CLASSIFICATION: 536
PRIOR APPLICATION STAN:

APPLICATION NUMBER: US/08/393,439
FILING DATE: 23-FEB-1995
PRIOR APPLICATION NUMBER: US 08/047,860
FILING DATE: 13-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: SANDBERG, VICTORIA A.

REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 220.00010140
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: 612-305-1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 10; DB 3; L
100.0%; Pred. No. 1.9e+03;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                      ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-SOFTWARE: Patentin Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 53 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
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Best Local Similarity
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Sequence 41, Application US/09569344

Patent No. 6368802

GENERAL INFORMATION:

APPLICANT: UNIVERSITY OF ROCHESTER

TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS: 72
ADDRESSE: MUETING, RAASCH & GEBHARDT, P.A.
STREET: 119 No. 6368802th Fourth Street, Suite 201
CITY: Minneapolis
STATE: Minnesota
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 10; DB 4; Length 53; 30.0%; Pred. No. 1.9e+03; tive 7; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                     Length 53;
                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/805,631
FILING DATE: 26-FEB-97
APPLICATION NUMBER: US 08/393,439
FILING DATE: 23-FEB-1995
APPLICATION NUMBER: US 08/047,860
PILING DATE: 15-APR-1993
ATTORNEY/AGENT INFORMATION:

NAME: SANDBERG, VICTORIA A.

REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 220.00010140
                                                                                                                                                                                                                                                                                                                                  100.0%; Score 10; DB 4; 1 100.0%; Pred. No. 1.9e+03;
                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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APPLICATION NUMBER: US/09/569,344
FILING DATE: 11.May-2000
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: RNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO: 41:
                                                                                                                                                     ;
TOPOLOGY: circular
;
MOLECULE TYPE: DNA (genomic)
;
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-569-344-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 612-305-1226
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LENGTH: 53 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 612-305-1228
                                    SEQUENCE CHARACTERISTICS:
LENGTH: 53 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
      INFORMATION FOR SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP; 55401
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 10v...
Local Similarity 10v...
Local Similarity 10v...
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Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-569-344-41
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US-09-569-344-40/C
US-09-569-344-40,C
; Sequence 40, Application US/09569344
; Patent No. 6386802
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF ROCHESTER
; TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
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ADDRESSE: MUETING, RAASCH & GEBHARDT, P.A.
STREET: 119 No. 6368802th Fourth Street, Suite 201
CITH: Minneapolis
STATE: Minnesota
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IN PC compatible
COMPUTER: IN PC compatible
COMPUTER: IN PC compatible
CORRATING SYSTEM: PC-DOS/MS-DOS
SOOTWARE: Patentin Release #1.0, Version #1.30
CURRENTCATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/569,344
FILING DATE: 11-May-2000
CLASSIFCATION AND ATA:
APPLICATION NUMBER: US 08/805,631
FILING DATE: 26-FEB-97
APPLICATION NUMBER: US 08/393,439
FILING DATE: 23-FEB-1995
APPLICATION NUMBER: US 08/047,860
FILING DATE: 15-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 53,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 10; DB 3; Length 53
Pred. No. 1.9e+03;
7; Mismatches 0; Indels
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REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 220.00010140
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1226
TELEPHONE: 612-305-1228
                                                           FILING DATE: 20. FEB-97

CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,439

FILING DATE: 23. FEB-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/047,860

FILING DATE: 15. APR-1993
ATTORNEY AGENT INFORMATION:
NAME: SANDBERG, VICTORIA A.
REGISTRATION NUMBER: 220.00010140

TELEPHONE: 612-305-1226
TELEPHONE: 61205-1226
TELEPHONE: 61205-1236
TELEPHONE: 612
UMBER: US/08/805,631A
26-FEB-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
30.0%; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 30.0
Matches 3; Conservative
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38 CUUCUCUUUU 47
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                APPLICATION NUMBER:
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; Patent No. 6194150
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: MUDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
NUMBER OF SEQUENCES: 2751
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE:
STREET: 613 West Fifth Street
STREET: 5114 4700
CITY: Los Angeles
STREET: California
STREET: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOSTWARE: FASESEQ VESSION 1.5
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/585,684B
FILING DATE: January 16, 1996
RICH APPLICATION DATA:
APPLICATION NUMBER: 60/000,951
FILING DATE: July 7, 1995
ATTORNEY, AGENT THORMATION:
NAME: WARDARY, RECHARD
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
TELECOMMULCATION INFORMATION:
TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OFERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTESQ VERSION 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                             ZIF: 90071
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
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                     ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 base pairs
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Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CTTCTCTTTT 10
CORRESPONDENCE ADDRESS
                                                                                     CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
US-08-585~684B-2710
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Sequence 2710, Application US/08585684B

Fatent No. S877021

GENERAL INFORMATION:

APPLICANT: Stinchcomb, Daniel T.

APPLICANT: Arguinces, Thale

APPLICANT: MCS-Niggen, James

TITLE OF INVENTION: METHOD AND REAGENT FOR THE

TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE

TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES

NUMBER OF SEQUENCES: 2751
                                                                                     RESULT 46
US-08-585-684B-2533/C
| Sequence 2533, Application US/08585684B
| Patent No. 5877021
| GENERAL INFORMATION:
| APPLICANT: Stinchcomb, Daniel T. APPLICANT: Or INVENTION: METHOD AND REAGENT FOR THE TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES NUMBER OF SEQUENCES: 2751
| CORRESPONDENCE ADDRESS: 2751
| STREET: Sai West Fifth Street
| STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/585,684B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PILING DATE: January 16, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/000, 951
FILING DATE: July 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INCORMATION FOR SEQ ID NO: 2533: SEQUENCE CHARACTERISTICS: LENGTH: 54 base - TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 54 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CTTCTCTTTT 10
  38 CUUCUCUUUU 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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US-08-585-684B-2533
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Fatent No. 6379924

GENERAL INFORMATION:
TITLE OF INVENTION: Improved Protein Expression Strains
TITLE OF INVENTION: Improved Protein Expression Strains
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS: 30
CORRESPONDENCE ADDRESS: 4
STREET: 1020 First Avenue
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: United States of America
ZIP: 19406-1310
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-COMPUTER: PSP PC-PS PC PSP PC-PS 
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Patent No. 5362865

GENERAL INFORMATION:
TITLE OF INVENTION: Enhanced Expression in Plants Using
TITLE OF INVENTION: No. 5362865-translated Leader Sequences
TUTLE OF INVENTION: No. 5362865-translated Leader Sequences
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janelle D. Strode, Monsanto Company, BB4F
STREET: 700 Chesterfield Parkway No. 5362865th
CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 10; DB 4; Length 70; 100.0%; Pred. No. 1.8e+03; tive 0; Mismatches 0; Indels
                                                                                                                   100.0%; Score 10; DB 3; Length 54; 100.0%; Pred. No. 1.9e+03;
                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/446,047A
FILING DATE: 15-Dec-1999
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
WOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "PCR primer"
                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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Best Local Similarity 100.0
Matches 10; Conservative
                                                                                                             Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 CTTCTCTTT 39
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                                                                                                                                                                                                                                                                                                13 CTTCTCTTT
                                 linear
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      STRANDEDNESS:
                              ; TOPOLOGY: ]
US-09-038-073-2710
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US-09-446-047A-1
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US-08-117-374-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 10; DB 3; L 100.0%; Pred. No. 1.9e+03; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585,684
APLICATION NUMBER: 08/585,684
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/038,073 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REPERENCE DOCKET NUMBER: 218/078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585,684
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2710:
                                                                                                                                                                                                                                                              TELEPHONE: (213) 949-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INPORMATION FOR SEQ ID NO: 2533
SEQUENCE CHARACTERISTICS:
LENGTH: 54 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (213) 955-0440
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Best Local Similarity 100.
Matches 10; Conservative
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STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
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US-08-597-325-5
Sequence 5, Application US/08597325
Patent No. 6018100
GENERAL INFORMATION:
TITLE OF INVENTION:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janelle D. Strode, Monsanto Company, BB4F
STREET: 700 Chesterfield Parkway No. 6018100th
STREET: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                      100.0%; Score 10; DB 1; Length 71; ilarity 100.0%; Pred. No. 1.8e+03; Conservative 0; Mismatches 0; Indels
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WRDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OSFWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: 08/597,325
APPLICATION NUMBER: US/08/597,325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AFFLACATE:
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/366,240
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Strode, Janelle D.
REGISTRATION NUMBER: 34,738
REFERENCE/DOCKET NUMBER: 38-21(10647)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-604
TELEFAX: (314)537-604
TELEFAX: (314)537-604
TELEFAX: (314)537-607
TEL
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                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 10, Conservative
LENGTH: 71 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CTTCTCTTTT 10
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Best Local Similarity
Matches 10; Conserv
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US-08-597-325-5
                                                                                                                                                                                     ; MOLECULB 13
US-08-280-263-5
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; Sequence 5, Application US/08280263
; Patent No. 5659122
; GENERAL INFORMATION:
    APPLICANT AUGLIA, Glenn D.
    TITLE OF INVENTION: No. 5659122-translated Leader Sequences
    TITLE OF INVENTION: No. 5659122-translated Leader Sequences
    NUMBER OF SEQUENCES: 2
    CORRESPONDENCE ADDRESS:
    ADDRESSE: Jamelle D. Strode, Monsanto Company, BB4F
    STREET: 700 Chesterfield Parkway No. 5659122th
    CITY: St. Louis
    STATE: Missouri
    CONNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/280,263
FILING DATE: 25-ULL-1994
CLASSIFICATION 1800
PROOR APPLICATION 1800
PROOF APPLICATIO
                                                               COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
GOMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/NO-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PILING DATE:
FILING DATE:
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REGISTRATION NUMBER: 34,738
REGISTRATION NUMBER: 38-21(10531)A
TREERENCE/DOCKET NUMBER: 38-21(10531)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38-21 (10531) A
                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: Strode, Janelle D.
REGISTRATION NUMBER: 34,738
REFERENCE/DOCKET NUMBER: 38-21
TELECOMMUNICATION INFORMATION:
TELEFAX: (314)537-624
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 71 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
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US-08-280-263-5
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US-08-117-374-5
         COUNTRY:
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WESULI 56

Sequence 6, Application US/08117374

Fatent No. 5362865

GENERAL INFORMATION:
APPLICANT: Austin, Glenn D.
TITLE OF INVENTION: Enhanced Expression in Plants Using
TITLE OF INVENTION: Enhanced Expression in Plants Using
TITLE OF INVENTION: Enhanced Expression in Plants Using
TITLE OF INVENTION: DO. 5362865-translated Leader Sequences
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janelle D. Strode, Monsanto Company, BB4F
STREET: 700 Chesterfield Parkway No. 5362865th
STREET: 700 Chesterfield Parkway No. 5362865th
STREET: 700 Chesterfield Parkway No. 5362865th
STREET: ALIANS STREET: Popty disk
COMPTER: EMP PC Compatible
COMPTER: IBM PC COMPATION:
COMPATIBLE
COMPTER: IBM PC COMPATION:
COMPATIBLE
COMP
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; Sequence 6, Application US/08280263
; Patent No. 5659122.
; GENERAL INFORMATION:
; TITLE OF INVENTION: Enhanced Expression in Plants Using
TITLE OF INVENTION: No. 5659122-translated Leader Sequences
; VUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janelle D. Strode, Monsanto Company, BB4F
; STRET: 700 Chesterfield Parkway No. 5659122th
; STRATE: Missouri
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Length 71;
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100.0%; Score 10; DB 5;
100.0%; Pred. No. 1.8e+03;
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MOLECULE TYPE: DNA (genomic)
US-08-117-374-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 75 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.

Best Local Similarity 100.
Matches 10; Conservative
Query Match 100.

Best Local Similarity 100.
Matches 10; Conservative
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TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 10; Conservative 0; Mismatches 0; Indels
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GENERAL INFORMATION:
TITLE OF INVENTION: Enhanced Expression in Plants Using
TITLE OF INVENTION: Non-translated Leader Sequences
NUMBER OF SEQUENCES: 2
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Re-bos/MS-DOS
                                                                                                                       ADDRESSEE: Janelle D. Strode, Monsanto Company, BB4F STREET: 700 Chesterfield Parkway No. 6018100th CITY: St. Louis
CITY: ASTER Missouri
COUNTRY: Wissouri
ZIP: 63198
APPLICANT: Rogers, Stephen G.
TITLE OF INVENTION: Promoter for Transgenic Plants
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFCATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/366,240
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Strode, Janelle D.
REGISTRATION NUMBER: 34,738
REFERENCE/DOCKET NUMBER: 38-21(10647) A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA: 08/597,325
APPLICATION NUMBER: US/08/597,325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10256
FILING DATE: 01-SEPT-1994
CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 71 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (344)537-6047
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 71 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CTTCTCTTT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US94-10256-5
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; Sequence 6, Application US/08597325
; Patent No. 6013100
; GENERAL INFORMATION:
; APPLICANT: Rogers, Stephen G.
; TITLE OF INVENTION: Promoter for Transgenic Plants
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS;
; ADDRESSEE: Janelle D. Strode, Monsanto Company, BB4F
; STREET: 700 Chesterfield Parkway No. 6018100th
; CITY: St. Louis
; CATATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 10; DB 3; Length 75; 100.0%; Pred. No. 1.8e+03; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                     Length 75;
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COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/597,325
                                                                                                                                                                                              100.0%; Score 10; DB 3; 1
100.0%; Pred. No. 1.8e+03;
ative 0; Mismatches 0;
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PRIOR APPLICATION:
PROCR APPLICATION DATA:
APPLICATION NUMBER: 08/366,240
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Strode, Janelle D.
REGISTRATION NUMBER: 34,738
REFERENCE/DOCKET NUMBER: 34,738
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-624
TELEFROME: (314)537-6047
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CRARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 60
PCT-US94-10256-6/c
; Sequence 6, Application PC/TUS9410256
                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-597-325-6
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                                                                                                                                                                         Query Match
Best Local Similarity 100...
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 75 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 10; Conservative
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EDNESS: double
                                                                TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-597-325-6/c
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Sequence 6, Application US/08597325

Patent No. 6018100

TITLE OF INVENTION:

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Janelle D. Strode, Monsanto Company, BB4F

STREET: 700 Chesterfield Parkway No. 6018100th

STATE: Missouri

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

Query Match

Best Local Similarity 100.0%; Pred. No. 1.8e+03;

Matches 10; Conservative 0; Mismatches 0; Indels
                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/280,263
FILING DATE: 25-UUL-1994
CLASSIFICATION: 800
PROOR APPLICATION NUMBER: US 08/117,374
FILING DATE: 02-SEP-1993
ATTORNEY/AGENT INFORMATION:
NUMBER: 02-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: 08/597,325
APPLICATION NUMBER: US/08/597,325
                                                                                                                                                                                                                                                                                                                     NAME: Strode, Janelle D.
REGISTRATION NUMBER: 34,738
REFRENCE/DOCKET NUMBER: 38-21(10531) A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6224
TELEPHONE: (314)537-6047
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 75 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATORNEY/AGENT INCEMATION:
NAME: Strode, Uanelle D.
REGISTRATION NUMBER: 34,738
REFERENCE/DOCKET NUMBER: 38-21(10647)A
TELEPHONE: (314)537-6224
TELEPHONE: (314)537-6224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/366,240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33 CTTCTCTTT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
  COUNTRY:
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Sequence 19, Application US/08280263

Patent No. 5659120

GENERAL INFORMATION:

APPLICANT: Austin, Glenn D.

TITLE OF INVENTION: No. 5659122-translated Leader Sequences

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS: 32

CORRESPONDENCE ADDRESS: January BB4F

STREET: 700 Chesterfield Parkway No. 5659122th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 10; DB 1; Length 78; 100.0%; Pred. No. 1.8e+03; Live 0; Mismatches 0; Indels
   Length 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enhanced Expression in Plants Using
Non-translated Leader Sequences
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MEDIUM TYPE: Floppy disk
COMPUTER: EN PC compatible
COMPUTER: EN PC compatible
COMPUTER: EN PC compatible
COMPUTER: EN PC compatible
CORRENT MATE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/280,263
FILING DATE: 25-JUL.1994
CLASSIFICATION NUMBER: US 08/117,374
APPLICATION NUMBER: US 08/117,374
APPLICATION NUMBER: 34,738
REGISTRATION NUMBER: 34,738
REGISTRATION NUMBER: 34,738
REGISTRATION NUMBER: 34,738
REGISTRATION INFORMATION:
TELEPHONE: (314)537-6224
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LEMETRY: 78 base pairs
LANDE: LANDE:
Query Match 100.0%; Score 10; DB 1; L
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 10; Conservative 0; Mismatches 0;
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COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
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MOLECULE TYPE: DNA (genomic)
US-08-280-263-19
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Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITCICITI 52
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 700 Chest
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
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PCT-US94-10256-19
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Sequence 19, Application US/08117374
Sequence 19, Application US/08117374
Patent No. 5362865
GENERAL INFORMATION:
APPLICANT: Austin, Glenn D.
TITLE OF INVENTION: Enhanced Expression in Plants Using
TITLE OF INVENTION: No. 5362865-translated Leader Sequences
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janelle D. Strode, Monsanto Company, BB4F
                           APPLICANT:
TITLE OF INVENTION: Enhanced Expression in Plants Using TITLE OF INVENTION: Non-translated Leader Sequences NUMBER OF SEQUENCES: 22
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PROFILE PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10256
FILING DATE: 01-SEPT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 10; DB 5; Length 75; 100.0%; Pred. No. 1.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 700 Chesterfield Parkway No. 5362865th COUNTRY: USA ZIP: MARCHIE WAS SIPERTED TO COUNTRY: USA ZIP: 63198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                             Enhanced Expression in Plants Using
Non-translated Leader Sequences
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/117,374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 Dase pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 75 base pairs
TYPE: mulleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 10; Conservative
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STRANDENNESS: double
TOPOLOGY: line...
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MEDIUM TYPE: Floppy
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      SENERAL INFORMATION:
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APPLICANT: Austin, Glenn D.
TITLE OF INVENTION: Bnhanced Expression in Plants Using
TITLE OF INVENTION: No. 5362865-translated Leader Sequences
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                               100.0%; Score 10; DB 5; Length 78; 100.0%; Pred. No. 1.8e+03; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Janelle D. Strode, Monsanto Company, BB4F STREET: 700 Chesterfield Parkway No. 5362865th CITY: St. Louis
             SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10256
FILING DATE: 01-SEPT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM FO Compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CARRENT APPLICATION DATA:
PILING DATE:
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PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20, Application US/08117374
Patent No. 5362865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Strode, Janelle D.
REGISTRATION NUMBER: 34,738
REFERENCE/DOCKET NUMBER: 38-21
TELECHONE: (314)537-624
TELEPHONE: (314)537-6047
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 82 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-117-374-20
                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                             FILING DATE: 01-SEPT-199-
CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 78 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
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CITY: St. Louis
STATE: Missouri
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40 CTTCTCTTTT
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US-08-117-374-20/c
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                                                                                                                                                                                                        TOPOLOGY:
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Enhanced Expression in Plants Using
No. 5659122-translated Leader Sequences
: 22
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GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Enhanced Expression in Plants Using
TITLE OF INVENTION: Non-translated Leader Sequences
NUMBER OF SEQUENCES: 22
COMPUTER READABLE FORM:
MEDIUM TYPE: FORM;
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER: PC-DOS/MS-DOS
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                                                                                                                                     APPLICANT: Austin, Glenn D.
TITLE OF INVENTION: Enhanced Expression in Plants Usi
TITLE OF INVENTION: Enhanced Expression in Plants Usi
TITLE OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSE: Janelle D. Strode, Monsanto Company, BB4
STREET: 700 Chesterfield Parkway No. 5659122th
CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER REAABLE FORM:

MEDIUM TYPE: Floppatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/280,263
FILING DATE: 25-JUL-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
PRING DATE: 02-SEP-1993
FILING DATE: 02-SEP-1993
ATTORNEY/AGENT INYORMATION:
NAME: Strode, Janelle D.
REGISTRATION NUMBER: 34-738
REFERENCE/DOCKET NUMBER: 38-21(10531)A
TELECOMMUNICATION INFORMATION:
TELEFRONE: (314)537-624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10256
FILING DATE: 01-SEPT-1994
US-08-280-263-20/c
; Sequence 20, Application US/08280263
; Patent No. 5659122
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CTTCTCTTT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCT-US94-10256-20/c
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FEATURE
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Sequence 11, Application US/09174465D

Fatent No. 6180364

GENERAL INFORMATION:

APPLICANT: KOMAN, Abnent

APPLICANT: CHASSIN, Dorine

APPLICANT: CHASSIN, Dorine

TITLE OF INVENTION: PREPARATION OF THIS PROTEIN AND PHARMACEUTICAL

TITLE OF INVENTION: PREPARATION OF THIS PROTEIN AND PHARMACEUTICAL

TITLE OF INVENTION: PROPERING CONTAINING SUCH, DNA CODING FOR SAID

TITLE OF INVENTION: PROTEIN

FILE REFERENCE: 017753-100

CURRENT APPLICATION NUMBER: US/09/174,465D

CURRENT FILING DATE: 1998-10-19

PRIOR APPLICATION NUMBER: US 08/482,842

NUMBER OF SEQ ID NOS: 16

SOFTWARE: PATENTING DATE: 1995-06-07

NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Application US/09599564A

Patent No. 6362318

GENERAL INFORMATION:
APPLICANT: KOMAN, Ahment
APPLICANT: CHASSIN, Dorine
APPLICANT: CHASSIN, Dorine
APPLICANT: BELLET, Dominique
TITLE OF INVENTION: NEW PROTEIN CALLED EPIL/PLACENTIN, PROCESS FOR THE
TITLE OF INVENTION: RORPOSITION OF THIS PROTEIN AND PHARMACEUTICAL
TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION: PROPERING
TITLE OF INVENTION OF PART 1200-05-23
CURRENT FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 09/174,465
PRIOR APPLICATION NUMBER: US 08/482,842
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COTHER INFORMATION: Description of Unknown Organism:EPIL - Early
CHER INFORMATION: Placenta Insulin-Like peptide
US-09-174-465D-11
                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 10; DB 3; Length 93; 100.0%; Pred. No. 1.8e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
LENGTH: 82 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Unknown
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US-09-599-564A-11/c
                                                                                                    ; MOLECULE 1151
PCT-US94-10256-20
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LENGTH: 93
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APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: Lo, Donald C.
APPLICANT: Lo, Donald C.
APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Puranam, Kasturi
APPLICANT: Farz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSEQ for Windows Version 4.0
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0
                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: (1)..(93)
COTHER INPORMATION: Description of Unknown Organism:EPIL - Early
COTHER INFORMATION: Placenta Insulin-Like peptide
US-09-599-564A-11
                                                                                                                                                                                                                                                                                                                                      ch 100.0%; Score 10; DB 4; Length 93; Similarity 100.0%; Pred. No. 1.8e+03; 10; Conservative 0; Mismatches 0; Indels
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APPLICANT: BAYER CORPORATION, The
APPLICANT: TAMBURINI, Paul P
APPLICANT: DAVIS, Gary
APPLICANT: DELARIA, Katherine A
APPLICANT: MULLER, Daniel K
APPLICANT: MULLER, Daniel K
TILLE OF INVENTION: HUMAN BIKUNIN
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 223, Application US/09461697; Patent No. 6277974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 55, Application US/09144428 ; Patent No. 6583108
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                        TYPE: DNA ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-461-697-223/c
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LENGTH: 96
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us-09-335-032-71.oli.rni

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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: Lo, Donald C.
APPLICANT: Lo, Donald C.
APPLICANT: Barney, Shawn
APPLICANT: Portbury, Stuart D.
APPLICANT: PORTBURY DEATH: DEATH
FILLE OF INVENTION: CELL DEATH
FILLE OF INVENTION: CELL DEATH
FILLE REPERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILLNG DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SSQ ID NOS: 466
SSQ ID NO 221
LENGTH: 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 10; DB 3; Length 112; 100.0%; Pred. No. 1.8e+03; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IP PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/932,082
FILING DATE: 12-AUG-1997
CLASSIFICATION NUMBER: 33,728
FILING DATE: 12-AUG-1997
CLASSIFICATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 34,311.204-US
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0123
INFORMATION CRARACTERISTICS:
LENGTH: 112 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 221, Application US/09461697 Patent No. 6277974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens US-09-461-697-221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-461-697-221/c
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US-09-461-697-219/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-932-082-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                COMPUTER READBRIE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,428
                                                                                                                                                                                                                                                                                                                                                                                 PILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/03894
FILING DATE: 10-MAR-1997
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,106
FILING DATE: 11-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/019,793
FILING DATE: 14-JUN-1996
PRIOR APPLICATION NUMBER: US 08/725,251
FILING DATE: 04-OCT-1996
ATPORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 37,293
FILENG DATE: 04-OCT-1996
ATPORNEY/AGENT INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10, Application US/08932082
Patent No. 6251856
GENERAL INFORMATION:
APPLICANT:
APPLICANT: Jonassen, Jan
APPLICANT: Brandt, Jakob
APPLICANT: Brandt, Jakob
APPLICANT: Rartzhals, Peter
APPLICANT: Rartzhals, Peter
APPLICANT: Kartzhals, Peter
APPLICANT: Kartzhals, Peter
APPLICANT: Kartzhals, Peter
APPLICANT: Kartzhals, 26
COMRESPONDENCE ADDRESS:
          : 300 S. Wacker Drive Suite 3200 CHICAGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 102 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
....hes 10; Conservative
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100.0%; Score 10; DB 3; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 10; DB 3; Length 146; 100.0%; Pred. No. 1.8e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,928A FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Remenick, James
REGISTRATION UNBER: 356902
REFERENCE/DOCKET NUMBER: 19060-0105
TELECOMMUNICATION INFORMATION:
TELEPAX: (202) 639 7700
TELEFAX: (202) 639 7700
TELEFAX: (202) 639 7890
INFORMATION FOR SEQ ID NO: 36: SEQUENCE CHARACTERISTICS:
LENGTH: 146 base pairs
TYPE: mucleic acid
TYPE: mucleic acid
                                                                            STATE: California
COUNTRY: U.S.A.
ZIP. 2004-2400
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                  SEE: BAKER & BOTTS
1299 Pennsylvania Avenue
Washington D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.us
Toches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138 Cricicitir 129
    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
US-09-461-697-217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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MOLECULE TYPE:
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                                  APPLICANT: Barney, Shawn
APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Furanam, Kasturi
APPLICANT: Edward Compositions Compositions and METHODS FOR DIAGNOSING
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
UNRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSEQ for Mindows Version 4.0
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Sequence 22, Application US/09441416A

Sequence 22, Application US/09441416A

GENERAL INFORMATION:
APPLICANT: Porter, David A.
APPLICANT: Skolnik, Paul R.
TITLE OF INVENTION: CELL-PERMEABLE PROTEIN INHIBITORS OF TITLE OF INVENTION: CALPRIN CALPAIN
FILE REPERENCE: 00398-140001
CURRENT APPLICATION NUMBER: US/09/441,416A
CURRENT FILING DATE: 1990-11-16
PRIOR FILING DATE: 1997-11-04

NUMBER OF SEQ ID NOS: 23
SOCTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 132
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Patent No. 6207389
GENERAL INFORMATION:
APPLICANT: Dosch, Hans M.
TITLE OF INVENTION: METHODS FOR CONTROLLING T
TITLE OF INVENTION: LYMPHOCYTE MEDIATED IMMUNE RESPONSES
NUMBER OF SEQUENCES: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
COGENT NEUROSCIENCE, Inc
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Best Local Similarity 100.
Marches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98 Cricicitri 89
                      Lo, Donald C
                                                                                                                                                                                                                                                                                                                              TYPE: DNA
CORGANISM: Homo sapiens
US-09-461-697-219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)...(129)
US-09-441-416A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Eukaryote
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-477-928A-36/c
                                                                                                                                                                                                                                                                                          SEQ ID NO 219
LENGTH: 126
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APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Thomas, Mary Beth
APPLICANT: Puranam, Kasturi
APPLICANT: Puranam, Kasturi
APPLICANT: Puranam, Kasturi
APPLICANT: ARIZ, Lawrence
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: CELL DEATH
TITLE DEATH
TITLE OF INVENTION: CELL DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 10; DB 3; Length 195; 100.0%; Pred. No. 1.8e+03; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTE: MASSACHUSEUS

ZIP: 02554

COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660

COMPUTER: PC
COMPUTER: PC
COMPUTER: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A

FILING DATE: 30-Jun-1998

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/085,598

FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                               Sequence 211, Application US/09461697
Patent No. 6277974
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (781)893-5007
TELEPRA: (781)893-8277
INFORMATION FOR SEQ ID NO: 2918:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.

Best Local Similarity 100.

Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 CTTCTCTTTT 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-461-697-211
      RESULT 79
US-09-461-697-211/c
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APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: Lo, Donald C.

APPLICANT: Barney, Shawn
APPLICANT: Homas, Mary Beth
APPLICANT: Portbury, Stuart D.
APPLICANT: Puramen, Kasturi
APPLICANT: NEURATION: COMPOSITIONS AND METHODS FOR DIAGNOSING
ITILE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
ITILE OF INVENTION: CELL DEATH
FILE REPERENCE: 10001-005-999
CURRENT APPLICANTION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOTTWARE: FREESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: Lo, Donald C.
APPLICANT: Lo, Donald C.
APPLICANT: Lo, Donald C.
APPLICANT: Harney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Purname, Kasturi
APPLICANT: Purname, Kasturi
APPLICANT: Katz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
TITLE OF INVENTION: CELL DEATH
FILE REPERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 10; DB 3; Length 18:
100.0%; Pred. No. 1.80+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 213, Application US/09461697
Patent No. 6277974
GENERAL INFORMATION:
                                                                                                                                                    Sequence 215, Application US/09461697
Patent No. 6277974
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146 CTTCTCTTTT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161 CTTCTCTTT 152
      128 CTTCTCTTT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CITCICITII 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-461-697-215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                        RESULT 77
US-09-461-697-215/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-461-697-213/c
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LENGTH: 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 215
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RESULT 82
US-09-107-532A-3253/C
is Sequence 3253, Application US/09107532A
j Patent No. 6583275
j Patent No. 6883275
j Patent No. 1 Doucette-Stamm and David Bush
j APPLICANT: Lynn A Doucette-Stamm and David Bush
j TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: PATENCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                              100.0%; Score 10; DB 4; Length 201; 100.0%; Pred. No. 1.8e+03;
                                                                                                                                                         Indels
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APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
NAME/KEY: misc_feature
;
LOCATION: (B) LOCATION 1...201
;
SEQUENCE DESCRIPTION: SEQ ID NO: 3253:
US-09-107-532A-3253
                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
;
SEQUENCE DESCRIPTION: SEQ ID NO: 439:
US-09-107-532A-439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 3253:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Massachusetts
                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMBUTER: PC
COPERATING SYSTEM: «Unknown>
SOFWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
FILING DATE: 14 MAY 1998
APPLICATION NUMBER: 60/051571
                                                                                                                                                                                                                          NAME/KEY: misc_feature

LOCATION: (B) LOCATION 1...198

SEQUENCE DESCRIPTION: SEQ ID NO: 2918:
US-09-107-532A-2918
                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY DARE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GFC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Enterococcus faecium
                                                                                                                                                    ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 100 Beaver Street
CITY: Waltham
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                                                                                     TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
               LENGTH: 198 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (781)893-8277
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 CTTCTCTTTT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CTTCTCTTTT 10
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -09-107-532A-439
                                                                                                                                                                                                                      FEATURE
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Gaps

FEATURE:

Matches

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Sequence 99, Application US/09016434
Patent No. 6500393
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
CARRESPONDENCE ADDRESS:
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
5217891-19/c
;Patent No. 5217891
APPLICANT: BRAKE, ANTHONY J.;VAN DEN BERG, JOHAN A.
TITLE OF INVENTION: DNA CONSTRUCTS CONTAINING A KLUTVEROMYCES
;A FACTOR LEADER SEQUENCE FOR DIRECTING SECRETION OF HETEROLOGOUS
;POLYPEPTIDES
;POLYPETIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 10; DB 6; Length 222; 100.0%; Pred. No. 1.8e+03; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: PLOPPY disk
COMPUTER: PLOPPY DESCRIPTION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
CLASSIFICATION:
                                                                                                                                                                                                  NUMBER OF SEQUENCES: 23
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/507,398
FILING DATE: 09-APR-1990
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 78,551
FILING DATE: 28-JUL-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PA-0002 US
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ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRANION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-01
TELECOMMUNICATION INFORMATION:
TELEFAX: (650) 855-0555
TELEFAX: (650) 855-0555
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         228 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CTICICITIT 10
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CLONE: 1251228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 86
US-09-016-434-99/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO:19:
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APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: Lo, Donald C.
APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart D.
APPLICANT: Puranam, Kasturi
APPLICANT: Puranam, Kasturi
APPLICANT: Ratz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: COMPOSITIONS DISORDERS, OR DISEASES INVOLVING
TITLE OF INVENTION: CELL, DEATH
FILLE REPERBRUCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT PILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SEQ ID NO 209
LENGTH: 213
                                                                                                             Sequence 7004, Application US/09313294A
Patent No. 6476212
GENERAL INFORMATION:
GANGATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Sherman:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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AND NO TOWN EAR
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature OTHER INFORMATION: Incyte ID No. 6476212 700380982H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: unsure
LOCATION: 190, 193
OTHER INFORMATION: a, t, c, g, or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 209, Application US/09461697
Patent No. 6277974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CTTCTCTTTT 10
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Zea mays
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                                                             RESULT 83
US-09-313-294A-7004
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US-09-016-434-99

RESULT 85

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APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 10; DB 4; Length 23
100.0%; Pred. No. 1.8e+03;
live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COPERATING SYSTEM: «Unknown»
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature; LOCATION: (B) LŌCATION 1...231; SEQUENCE DESCRIPTION: SEQ ID NO: 2834: US-09-107-532A-2834
   ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40.489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
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US-09-107-532A-724/c
'Sequence 724, Application US/09107532A
'Patent No. 6583275
'GENERAL INFORMATION'
                                                                                                                                                                                         TELEPHONE: (781)893-5007
TELEPK: (781)893-8277
INFORMATION FOR SEQ ID NO: 2834:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                     LENGTH: 231 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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COUNTRY: USA
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Best Local Similarity 100.
Matches 10; Conservative
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APPLICANT: Lo, Donald C.
APPLICANT: Lo, Donald C.
APPLICANT: Barney, Shawn
APPLICANT: Barney, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Wasturi
APPLICANT: Wasturi
APPLICANT: WORNTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: COMPOSITIONS AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT PILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOCTION OF SECULOR OF SECULOR
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                                100.0%; Score 10; DB 4; Length 228; 100.0%; Pred. No. 1.8e+03; Live 0; Mismatches 0; Indels
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
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FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
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MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-107-532A-2834/c
; Sequence 2834, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
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OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                         Sequence 207, Application US/09461697 Patent No. 6277974
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COUNTRY: USA
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Query Match
Best Local Similarity 100...
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Best Local Similarity 100.
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                                                                                                                                                            1 CTTCTCTTTT 10
                                                                                                                                                                                                                   58 Cricicitii 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-09-461-697-207
                                                                                                                                                                                                                                                                                                              RESULT 87
US-09-461-697-207/c
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LENGTH: 231
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WS-09-433-826B-360

Sequence 360, Application US/09433826B

Patent No. 6579973

GENERAL INFORMATION:
APPLICANT: Jiang, Yuqui
APPLICANT: Dillion, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Matcham, Jennifer L.
APPLICANT: Willion, Davin C.
TITLE OF INVENTION: COMOSITIONS
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.470C4
CURRENT APPLICATION NUMBER: US/09/433,826B

CURRENT APPLICATION NUMBER: US/09/433,826B

CURRENT FILING DATE: 1999-11-03

NUMBER OF SEQ ID NOS: 474

SEQ ID NO 360

LENGTH: 241
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APPLICANT: Jiang, Yuqiu
APPLICANT: Jiang, Yuqiu
APPLICANT: Jiang, Yuqiu
APPLICANT: Miccham, Jannifer L.
APPLICANT: Miccham, Jannifer L.
APPLICANT: Mariocker, Susan L.
APPLICANT: Hepler, William T.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.47006
CURRENT FILING DATE: 2000-07-20
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 495
SOFTWARE: FREESEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-620-405B-360
; Sequence 360, Application US/09620405B
; Patent No. 6528054
                                                 ; NAME/KEY: misc_feature
; LCCATION: (1)...(241)
; OTHER INFORMATION: n = A,T,C or G
US-09-389-681-360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (1)...(241)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                  113 CTTCTCTTT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 Cricicitrii 122
                                                                                                                                                                                                                                                                                1 CTTCTCTTTT 10
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
  ORGANISM: Homo sapiens
FEATURE:
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LENGTH: 241
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Sequence 360, Application US/09389681A

Patent No. 6518237

GENERAL INFORMATION:

APPLICANT: Width, Jang

APPLICANT: Mitcham, Jennifer L.

APPLICANT: MINER SERBENCE: 210121.470C3

FILE REFERENCE: 210121.470C3

CURRENT APPLICATION NUMBER: US/09/389,681A

CURRENT FILING DATE: 1999-09-02

NUMBER OF SEQ ID NOS: 463

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 360

LENGTH: 241

TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                         Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NESULT 90-397-787-56

Sequence 56, Application US/09397787

Patent No. 6468768

GENERAL INFORMATION:
APPLICANT: Benson, Darin R.
APPLICANT: Lodes, Michael J.
APPLICANT: Mitchael J.
APPLICANT: Michael J.
APPLICANT: Mitchael J.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR OVARIAN
TITLE OF INVENTION: CANCER THERAPY AND DIAGNOSIS
FILE REFERENCE: 210121.466C2
CURRENT APPLICATION UNBER: US/09/397,787
CURRENT APPLICATION NUMBER: US/09/397,787

NUMBER OF SEQ ID NOS: 334

SOUTHWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 56

LENGTH: 241
                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 10; DB 4; I
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 10; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...234
SEQUENCE DESCRIPTION: SEQ ID NO: 724:
                                            TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
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CORGANISM: Homo sapien
US-09-397-787-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CTTCTCTTTT
                                                                                                                                                                                                                                                                                                     US-09-107-532A-724
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US-09-389-681-360
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100.0%; Score 10; DB 4; Length 247; 100.0%; Pred. No. 1.8e+03; ative 0; Mismatches 0; Indels
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5 Sequence 9, Application US/09098789
5 Patent No. 6180342
5 Patent No. 6180342
5 Patent No. 6180342
6 Patent No. 6180342
6 Patent No. 618034
6 Patent
         OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
SOCTWRENT APPLICATION NUMBER: US/09/016,434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER FEDDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/098,789
                                                                                                                                                                     FILING DATE: HERENTH CS/09/010,434
CLASSIPECATION:
PRIOR APPLICATION:
PRIOR APPLICATION:
APPLICATION NUMBER:
FILING DATE:
CLASSIPTCATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REFERENCE/DOCKET NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
FELECOMMUNICATION INFORMATION:
TELEFAX: (650) 845-1166
INFORMATION FOR SEQ ID NO: 737:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 base pairs
TYPE: nucleic acid
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NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REPERENCE/DOCKET NUMBER: PF-0547 US
TELECOMMINICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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; CLONE: 395476
US-09-016-434-737
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Best Local Similarity
Matches 10; Conserv
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IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Jiang, Yugiu
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun
APPLICANT: Harlocker, Susan L.
APPLICANT: Hepler, William T.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DILANOSIS OF BREAST CANCER
FILE REFERENCE: 210121.470c7
CURRENT APPLICATION NUMBER: US/09/604,287A
CURRENT FILING DATE: 2000-06-22
NUMBER OF SEQ 1D NOS: 489
SOFTWARE: FastSEQ for Windows Version 3.0
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Patent No. 6500338

GENERATION: GARGATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
ITILE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
ITILE OF INVENTION: PATHWAY GENE EXPRESSION
CORRESPONDENCES: 1490
CORRESPONDENCE ADDRESS: ADDRESSEE: ADD
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100.0%; Score 10; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 10; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 360, Application US/09604287A Patent No. 6586572 GENERAL INFORMATION:
                                                                              NAME/KEY: misc_feature

| LOCATION: (1)...(241)

| CTHER INFORMATION: n = A,T,C or G

US-09-433-8268-360
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; OTHER INFORMATION: n = A,T,C or G
US-09-604-287A-360
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: PALO ALTO STATE: CALIFORNIA
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US-09-016-434-737/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 94
US-09-604-287A-360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 360
LENGTH: 241
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Gaps

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RESULT 100

US-09-134-001C-18/C

Sequence 18, Application US/09134001C

PREENT NO. 6380370

GENERAL INFORMATION:

TITLE OF INVENTION: WILLIAM AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS: TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT PELING DATE: 1998-08-13

PRIOR FILING DATE: 1998-08-13

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-08-14

SEQ ID NOS: 5674

LENGTH: 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Laigudi, Raghunath V.
APPLICANT: Laigudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: U$/09/313,294A
CURRENT FILE OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 3143
LEWART: A.
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                                                                                                                                                                                                                                                         Length 256;
                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
CTHER INFORMATION: Incyte ID No. 6476212 700610958H1
NAME/KEY: unsure
CACATION: 216, 246
COTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-3143
                                                                                                                                                                                                                                                     100.0%; Score 10; DB 4; 1
100.0%; Pred. No. 1.7e+03;
iive 0; Mismatches 0;
      FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 99
US-09-313-294A-3143/c
; Sequence 3143, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                              TYPE: DNA
CORGANISM: Homo sapien
US-09-736-457-1077
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                                                                                                                   SEQ ID NO 1077
LENGTH: 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Carter, Cary
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Retter, Darrick
APPLICANT: Retter, Darrick
APPLICANT: Pan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C14
CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 1833
SOFFWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Wang, Aljun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
                                                                                                                                                                                                                                                                                                0
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Patent No. 6504010
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
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Bangur, Chaitanya S.
Lodes, Michael A.
| INFORMATION FOR SEQ ID NO. 9-
| SEQUENCE CHARACTERISTICS:
| LENGTH: 251 base pairs
| TYPE: nucleic acid
| STRANDEDENESS: single
| TOPOLOGY: linear
| IMMEDIATE SOURCE:
| LINEARY: HIPONONO2
| CLONE: 2246348CT1
| US-09-098-789-9
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Vedvick, Tom
Carter, Darrick
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APPLICANT: Bangur,
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; TYPE: DNA; Cachalism: Staphylococcus epidermidis
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Query Match
Best Local Similarity 100.0%; Score 10; DB 4; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTTCTCTTT 10
Db 159 CTTCTCTTT 150
Search completed: October 28, 2003, 18:20:35
Job time: 96 secs
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Title: Perfect score: Sequence:

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257 10 US-09-969-373-534 259 9 US-09-864-761-17354 259 11 US-09-810-009A-276 260 10 US-09-910-009A-276 261 10 US-09-913-594-3894 261 10 US-09-913-876-631 262 11 US-09-913-876-631 263 11 US-09-913-876-631 263 11 US-09-913-876-631 263 11 US-09-913-876-631 264 10 US-09-913-874-13953 265 11 US-09-913-874-13953 265 11 US-09-913-874-1398 265 11 US-09-913-854-1398 266 11 US-09-913-854-1398 267 10 US-09-913-854-1398 266 11 US-09-913-854-1398 267 10 US-09-913-854-1398 268 10 US-09-878-574-1422 269 10 US-09-878-574-1422 260 10 US-09-878-574-1422 260 10 US-09-878-574-1422 261 10 US-09-878-574-1422 262 11 US-09-878-574-1422 263 10 US-09-878-574-14456 264 10 US-09-878-574-14499 265 10 US-09-878-574-1499 267 10 US-09-878-574-1499 277 10 US-09-878-574-1499 278 10 US-09-878-574-1499 279 10 US-09-878-574-1690 271 10 US-09-878-574-1690 271 10 US-09-878-574-1690 272 10 US-09-878-574-1690 273 10 US-09-878-574-1690 273 10 US-09-878-574-1690 274 10 US-09-878-574-1690 275 10 US-09-878-574-1690 277 10 US-09-878-574-1690 278 10 US-09-878-574-1690 279 10 US-09-878-574-1690 271 10 US-09-878-574-1690 271 10 US-09-878-574-1690 272 10 US-09-878-574-1690 273 10 US-09-878-574-1690 273 10 US-09-878-574-1690 274 10 US-09-878-574-1690 275 10 US-09-878-574-1690 277 10 US-09-878-574-1690 278 10 US-09-878-574-1690 279 10 US-09-878-574-1690 271 10 US-09-878-574-1690 271 10 US-09-878-574-1690 272 10 US-09-878-574-1690 273 10 US-09-878-574-1690 274 10 US-09-878-574-1690 275 10 US-09-878-574-1690 277 10 US-09-878-574-1690 278 10 US-09-878-574-1690 279 10 US-09-878-574-1690 271 10 US-09-878-574-1690 271 10 US-09-878-574-1690 272 10 US-09-878-574-1690 273 10 US-09-878-574-1690 274 10 US-09-878-574-1690 275 10 US-09-878-574-1690 277 10 US-09-878-574-1690 278 10 US-09-878-574-1690 279 10 US-09-878-574-1690 279 10 US-09-878-574-1690 279 10 US-09-878-574-1690 279 10 US-09-878-574-1690 270 10 US-09-878-574-1690 270 10 US-09-878-574-1690 271 10 US-09-878-574-1690 271 10 US-09-878-574-1690 272 10 US-09-878-574-1690 273 10 US-09-878-574-1690 274 10 US-09-878-574	4444444444
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Sequence 224, App Sequence 3072, Ap Sequence 245, App Sequence 224, App Sequence 224, App	Sequence 224, App Sequence 1955, Ap	Sequence 224, App Sequence 4429, Ap	Sequence 10732, A Sequence 224, App	Sequence 224, App	Sequence 151, App	Sequence 6771, Ap	Sequence 1209, Ap	Sequence 45, Appl	Sequence 300, APP Sequence 1667, Ap	Sequence 1838, Ap	Seguenc	Sequence 664, App	Sequence 7040, Ap	Sequence 899, App	Sequence 2070, Ap	Sequence 180, App	Sequence 1129, Ap	Sequence 1129, Ap	Sequence 8778, Ap	Sequence 254, App Sequence 285358,	Sequence 24244, A	Sequence 446, App Sequence 470, App	Sequence 110, App	Sequence 4005, Ap Sequence 10314, A	Sequen	Sequence 926, App Sequence 1635, Ap	Sequen	Sequence 26, Appl Sequence 3102, Ap	Sequence 6576, Ap	Sequence 288453, Sequence 6576, Ap	Sequence 8266, Ap	Sequence 7, Appli	Sequence 1668, Ap Sequence 17973, A	Sequence 7, Appli	Sequence 963, App	Sequence 1565, Ap	Sequence 168, App	Sequence 423, App	Seguen	Sequence 314, App Sequence 18543, A	Seguence 589, App	Sequence 100', Ap Sequence 81, Appl	Sequence 134, App	equenc	Adv. At Common C
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; Sequence 290, Application US/09827998
; Patent No. US30020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TILES OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILER REFERENCE: MDIMORE-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
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APPLICANT: GU, Yizhong

APPLICANT: GHANDON, MOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E

TITLE OF INVENTION: NOVEL 18/09/827,998

CURRENT APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR PRILING DATE: 2000-09-27

NUMBER OF SEQ ID NOS: 1881

SOFTWARE ABOMICA SEQUENCE Listing Engine

SEQ ID NO 291

LENGTH: 17
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| Patent NO. US20020102252A1
| GENERAL INFORMATION:
| APPLICANT: Shannon, Mark
| TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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100.0%; Score 10; DB 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 10; Conservative 0; Mismatches 0;
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Best Local Similarity 100.
Matches 10; Conservative
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US-09-827-998-292/c
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LENGTH: 17
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                                                                                                                                                                                                                                                 Sequence 288, Application US/09827998

Patent No. US20020102252A1

GENERAL INFORMATION:

APPLICANT: Gu, Yizhong

APPLICANT: Shannon, Mark

TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E

FILE REFERENCE: MDAMORE-8

CURRENT PILING DATE: 2001-04-06

PRIOR APPLICATION NUMBER: US/09/827,998

CURRENT FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

NUMBER OF SEQ ID NOS: 1881-

SOFTWARE: Aeomica Sequence Listing Engine

SEQ ID NO 288

LENGTH: 17
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Patent No. US20020102252A1

GENERAL INFORMATION:

APPLICANT: GLY, Yizhong

APPLICANT: Shannon, Mark

TILLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E

FILE REPERENCE: MDANORF-8

CURRENT APPLICATION NUMBER: US/09/827,998

CURRENT APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

NUMBER OF SEQ ID NOS: 1881

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Best Local Similarity 100.0%; Pred. No. 1.6e+04;

Matches 10; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 10; Conservative 0; Mismatches 0;
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US-09-827-998-289
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US-09-827-998-288
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US-09-827-998-288/c
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LENGTH: 17
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Sequence 1740, Application US/09930423

Fublication No. US20030092003A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Blatt, Larry

APPLICANT: Blatt, Larry

APPLICANT: Blatt, Larry

APPLICANT: McSwiggen, Jim

TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease;
FILE REFERENCE: MBHB00, 918-A 400/027

CURRENT APPLICATION NUMBER: 2001-08-15

NUMBER OF SEQ ID NOS: 4553

SOFTWARE: Patentin version 3.0

SEQ ID NO 1740

LENGTH: 17
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APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
TILLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
FILE REFERENCE: MEHBOO, 918-4400/027
CURRENT APPLICATION NUMBER: US/09/930,423
CURRENT APPLICATION NUMBER: US/09/930,423
SOFTWARE: PatentIn version 3.0
SEQ ID NOS: 4553
SOFTWARE: PatentIn version 3.0
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                                                                                                                                             Length 17;
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Matches 10; Conservative
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US-09-930-423-1741
                                               ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-294
                                                                                                                                                                                                                                                                                10 CTICICITIT 1
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ORGANISM: Homo Sapiens
US-09-930-423-1740
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Best Local Similarity
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  ; SEQ ID NO 294
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Sequence 293, Application US/09827998

Patent No. US20020102252A1

GENERAL INFORMATION:

APPLICANT GU, Yizhong

APPLICANT: Shannon, Mark

TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E

FILE REPRESENCE: MDHOMER: US/09/827,998

CURRENT APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-27

NUMBER OF SEQ ID NOS: 1881

SOFTWARE: Acomica Sequence Listing Engine

SEQ ID NO 293

LENGTH: 17
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Patent No. US20020102252a1

General INFORMATION:
APPLICANT: Gu, Yizhong
APPLICANT: Ghannon, Mark
ITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
FILE REPERENCE: MDRNORF-8

CURRENT APPLICATION NUMBER: US/09/827,998

CURRENT APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-09-27

NUMBER OF SEQ ID NOS: 1881

SOFTWARE: Aeomica Sequence Listing Engine
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Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 10; Conservative 0; Mismatches 0;
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                 CURRENT APPLICATION NUMBER: US/09/827,998
CURRENT FILING DATE: 2001-04-06
FRIOR APPLICATION NUMBER: US 60/207,456
FRIOR FILING DATE: 2000-05-26
FRIOR APPLICATION NUMBER: US 60/236,359
FRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 1881
SOFTWARE: Acomica Sequence Listing Engine
SOFTWARE: Acomica Sequence Listing Engine
LENGTH: 17
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FILE REFERENCE: MDhMORF-8
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                                                                                                                                                                                                                                                          TYPE: DNA
CORGANISM: Homo sapiens
US-09-827-998-292
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US-09-827-998-293
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Best Local Similarity
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US-09-827-998-294/c
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Sequence 1721, Application US/10060756A

Publication No. US20030046717A1

GENERAL INFORMATION:

APPLICATT: Zhang, Jian

TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
FILE REPERENCE: PB0177

CURRENT APPLICATION NUMBER: US/10/0667

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR PLING DATE: 2001-01-30

PRIOR PPLICATION NUMBER: PCT/US01/00668

PRIOR PLING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/327,898

PRIOR APPLICATION NUMBER: US 60/327,898
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                                                PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION UNMBER: PCT/USO1/00665
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-05-33
PRIOR FILING DATE: 2001-05-33
PRIOR FILING DATE: 2001-06-93
NUMBER: OF SEQ ID NOS: 4804
SEQ ID NO 1720
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US-10-060-756A-1720
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Best Local Similarity
Matches 10; Conserv
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US-10-060-756A-1721/c
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US-10-060-756A-1722/c
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US-09-745-237A-1740/c

19-09-745-237A-1740/c

19-09-746-237A-1740/c

19-09-746-237A-1740/c

19-09-746-237A-1740/c

19-09-746-237A-1740/c

19-09-746-237A-1740/c

19-09-746-237A-1740/c

19-09-746-237A-1740/c

19-09-740-237A-1740/c

19-09-740-237A-1740/c

19-09-74-15/c

19-09-74-15/c

19-09-74-15/c

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19-09-74-15/c

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19-09-74-16/c

19-09-74
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Publication No. US20030143708A1
GENERAL INFORMATION:
APPLICANT: Blatt, Larry
APPLICANT: McSuggen, Jim
TITLE OF INVENTION: Mcthod and Reagent for the Treatment of Alzheimer's Disease
FILE REFERENCE: 400/007 (MBHB00-918-A)
CURRENT FILING DATE: 2002-04-15
NUMBER OF SEQ ID NOS: 4550
SOFTWARE: Patentin version 3.0
LENGTH: 17
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| Publication No. US20030046717A1
| GENERAL INFORMATION:
| APPLICANT: Zhang, Jian
| TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
| FILE REPERENCE: PB0177
| CURRENT APPLICATION NUMBER: US/10/060,756A
| CURRENT FILING DATE: 2002-01-30
| PRIOR APPLICATION NUMBER: PCT/US01/00667
| PRIOR APPLICATION NUMBER: PCT/US01/00664
| PRIOR APPLICATION NUMBER: PCT/US01/00664
| PRIOR APPLICATION NUMBER: PCT/US01/00669
| PRIOR APPLICATION NUMBER: PCT/US01/00669
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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CORGANISM: Homo sapiens
US-09-745-237A-1740
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CORGANISM: Homo sapiens
US-09-745-237A-1741
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Sequence 1724, Application US/10060756A

Publication No. US20030046717A1

GENERAL INFORMATION:

APPLICAT': Zhang, Jian

TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN

FILLE REPRENCE: PBD177

CURRENT APPLICATION NUMBER: US/10/0667

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30
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Publication No. US20030046717A1
GENERAL INFORMATION:
APPLICATION NO. US20030046717A1
GENERAL INFORMATION:
I TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
FILE REFERENCE: P80177
CURRENT FILING DATE: 2002-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR PAPLICATION NUMBER: PCT/US01/00664
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
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100.0%; Score 10; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                  Length 17;
                                                                                                             100.0%; Score 10; DB 14; 100.0%; Pred. No. 1.6e+04;
                                                                                                                                                                                                         0; Mismatches
                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
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                      US-10-060-756A-1723
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TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
FILE REPERENCE: PB0177
CURRENT APPLICATION NUMBER: US/10/060,756A
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR PLING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR PLING DATE: 2001-01-30
Sequence 1722, Application US/10060756A

Publication No. US2030046717A1
GENERAL INFORMATION:
APPLICANT: Zhang, Jian
TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
FILE REFERRINCE: P80177
CURRENT FILING DATE: 2002-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PAPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-05-23
PRIOR PLING DATE: 2001-05-33
PRIOR PLING DATE: 2001-05-30
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100.0%; Pred. No. 1.6e+04;
tive 0; Mismatches 0;
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; Sequence 1723, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 10; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-1722
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, Sequence 609, Application US/10205309
, Publication No. US20030190635A1
, GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 10; Conservative
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US-10-205-309-609
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| Sequence 1726, Application US/10060756A
| Publication No. US20030046717A1
| GENERAL INFORMATION:
| APPLICANT: Zhang, Jian
| TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
| FILE REPERBENCE: PB0177
| CURRENT FILING DATE: 2002-01-30
| PRIOR APPLICATION NUMBER: US/10/00667
| PRIOR PPLING DATE: 2001-01-30
| PRIOR PLING DATE: 2001-01-30
| PRIOR PLING DATE: 2001-01-30
| PRIOR PLING DATE: 2001-01-30
| PRIOR PILING DATE: 2001-01-30
| PRIOR PLING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 10; DB 14; Length 17; 100.0%; Pred. No. 1.6e+04; tive 0; Mismatches 0; Indels
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION UNBER: PCT/USO1/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APLICATION NUMBER: US 09/864,761
PRIOR FILING DATE: 2001-05-23
PRIOR FILING DATE: 2001-05-23
PRIOR FILING DATE: 2001-10-09
NUMBER OF SEQ ID NOS: 4804
SOFTWARE: Acomica Sequence Listing Engine
SEQ ID NO 1725
LENGTH: 17
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SEQ ID NO 1726
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-10-060-756A-1727/c
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US-10-205-309-284/c

Sequence 284, Application US/10205309

Sequence 284, Application US/10205309

Sequence 284, Application US/10205309

Publication No. US2030130635A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Definition of Alzheimer's Disease Usin TITLE OF INVENTION: Interfering RNA

FILE REFERENCE: 900/033

FURE REFERENCE: 900/033

CURRENT APPLICATION UNMER: US/10/205,309

CURRENT FILING DATE: 2002-10-25

NUMBER OF SEQ ID NOS: 674

SOSTWARE: PatentIn version 3.0
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TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
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                                                                    CURRENT APPLICATION NUMBER: US/10/060,756A
CURRENT FILING DATE: 2002-01-30
PRIOR PELING DATE: 2002-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLILOATION NUMBER: PCT/US01/00668
PRIOR PLILOATION NUMBER: PCT/US01/00668
PRIOR PLILOATION NUMBER: PCT/US01/00668
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-05-23
PRIOR PILING DATE: 2001-05-23
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-01-30
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US-10-438-729-167/c

Sequence 167, Application US/10438729

Sequence 167, Application US/10438729

Sequence 167, Application US/10438729

Sequence 167, Application US/10438729

THE REPERENCE OF INVENTION: METHODS OF SELECTING T CELL RECEPTOR V PEPTIDES FOR THERAPEUTIC

TITLE REPERENCE: 6315-65828

CURRENT APPLICATION NUMBER: US/10/438,729

CURRENT APPLICATION NUMBER: US/203,984

PRIOR APPLICATION NUMBER: 09/203,984

PRIOR PILING DATE: 2000-05-12

PRIOR APPLICATION NUMBER: 09/853,830

PRIOR PILING DATE: 2000-05-12

PRIOR PILING DATE: 2000-05-14

NUMBER OF SEQ ID NOS: 181

SEQ ID NO 167

LENGTH: 24
                                                                                                                                                                                                                                    US-09-934-489A-46/c

i Sequence 46, Application US/09934489A

i Publication No. US20330108872A1

i Publication No. US20330108872A1

i APPLICANT: Sulavik, Mark

i APPLICANT: Ling, Losee Lucy

i APPLICANT: Opperman, Tim

i APPLICANT: Mark

i TILE OF INVENTION: Genomics-Assisted Rapid Identification of Targets

i TILE PREBEROR: 032796-082

i CURRENT APPLICATION NUMBER: US/09/934,489A

i CURRENT APPLICATION NUMBER: US 60/226,896

i PRIOR PILING DATE: 2001-08-23

i NUMBER OF SEQ ID NOS: 63

i SOFTWARE: PastSEQ for Windows Version 4.0

i SEQ ID NO 46

i LENGTH: 24
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                              Length 24;
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                       100.0%; Score 10; DB 10;
100.0%; Pred. No. 1.6e+04;
cive 0; Mismatches 0;
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100.0%;
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ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) OTHER INFORMATION: synthetic US-10-438-729-167
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Best Local Similarity 100...
                       Query Match
Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity
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             APPLICANT: McSwiggen, James
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Alzheimer's Disease Using
TITLE OF INVENTION: Interfering RNA
FILE REPERENCE: 900/033
CURRENT APPLICATION NUMBER: US/10/205,309
CURRENT FILING DATE: 2002-10-25
NUMBER OF SEQ ID NOS: 674
SOFTWARE: Patentin version 3.0
SEQ ID NO 609
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: ESCATY, Jean-Louis
TITLE OF INVENTION: NEW POLYNUCLEOTIDES AND POLYPEPTIDES OF THE IFNalpha-2 GENE
FILE REPERENCE: 021349/0010
CURRENT APPLICATION NUMBER: US/10/087,325
CURRENT APPLICATION NUMBER: 2002-03-01
PRIOR APPLICATION NUMBER: FR 0102843
PRIOR APPLICATION NUMBER: FR 0102843
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.1
SEQ ID NO 15
LENGTH: 20
                                                                                                                                                                                                                                                                                       ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sinA antisense region
US-10-205-309-609
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US-09-563-830-168/C
; Sequence 168, Application US/09853830
; Patent No. US20020107388A1
; GENERAL INFORMATION:
; APPLICANT: VANGANDARK, Arthur A.
; TITLE OF INVENTION: Methods of Identifying and Monitoring; FILE REFERENCE: P-IM 4734
; CURRENT APPLICATION NUMBER: US/09/853,830
; CURRENT FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                  Length 19;
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100.0%; Pred. No. 1.6e+04;
tive 0; Mismatches 0;
APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15, Application US/10087325
Publication No. US20020192682A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                              TYPE: RNA
ORGANISM: Artificial Sequence
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Best Local Similarity 30.0.
Best Local 3; Conservative
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CORGANISM: Homo sapiens
US-09-853-830-168
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Best Local Similarity
Matches 10; Conserv
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LENGTH: 24
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Gaps

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Sequence 1104, Application US/09827998
PERENT US/0020102252A1
GENERAL INFORMATION:
APPLICANT: GLANGATION:
APPLICANT: Shannon, Mark
TILLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
FILE REFERENCE: WDDMORE-8
CURRENT APPLICATION NUMBER: US/09/827,998
CURRENT PILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PLING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PLING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 1881
SSEQ ID NO 1104
LENGTH: 25
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TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
FILE REFERENCE: MDHORF-8

CURRENT APPLICATION NUMBER: US/09/827,998

CURRENT FILING DATE: 2001-04-06

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

NUMBER OF SEQ ID NOS: 1881

SOFTWARE: Acomica Sequence Listing Engine

SEQ ID NO 1105

LENGTH: 25
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Parent No. US20020102252A1

GENERAL INFORMATION:
APPLICANT: Gu, Yizhong
APPLICANT: Shannon, Mark
TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN FILE REFERENCE: Whidher: US/09/827,998
CURRENT APPLICATION NUMBER: US/09/827,998
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100.0%; Pred. No. 1.6e+04;
iive 0; Mismatches 0;
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100.0%; Pred. No. 1.6e+04;
iive 0; Mismatches 0;
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Patent No. US20020102252A1
; GRNEAL INFORMATION:
; APPLICANT: Gu, Yizhong
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Best Local Similarity 100.
Matches 10; Conservative
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; ORGANISM: Homo sapiens
US-09-827-998-1105
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; ORGANISM: Homo sapiens
US-09-827-998-1104
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US-09-827-998-1105/c
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US-09-827-998-1106/c
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Fatent No. US20020102252A1
GENERAL INFORMATION:
APPLICANT: Gu, Yizhong
FILE REPERENCE: MDAMORE.
FILE REPERENCE: MDAMORE.
FILE REPERENCE: MDAMORE.
FRICRENT APPLICATION NUMBER: US/09/827,998
CURRENT APPLICATION NUMBER: US 60/207,456
FRICR APPLICATION NUMBER: US 60/207,456
FRICR APPLICATION NUMBER: US 60/205,359
                                                                                                                                                                                                      Sequence 1102, Application US/09827998

Petent No. US2002012252A1

GENERAL INFORMATION:

APPLICANT: GL, Yizhong

APPLICANT: GLannon, Mark

TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E

FILE REFERENCE: MDHWORF-8

CURRENT APPLICATION NUMBER: US/09/827,998

CURRENT APPLICATION NUMBER: US/09/827,998

CURRENT APPLICATION NUMBER: US/09/827,998

PRIOR PETING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-09-27

NUMBER OF SEQ ID NOS: 1881

SEQ ID NOS: 1881

SEQ ID NO 1102

LENGTH: 25
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       Mismatches
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Best Local Similarity 100...
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Matches 10; Conservative
    10; Conservative
                                                  1 CTICTCTITI 10
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25 CTTCTCTTTT 16
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                                                                                              18 CTTCTCTTT 9
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; ORGANISM: Homo sapiens
US-09-827-998-1102
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US-09-827-998-1102/c
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US-09-827-998-1103/c
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US-09-827-998-1104/c
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Sequence 1109, Application US/09827998
Sequence 1109, Application US/09827998
Sequence 1109, Application US/09827998
Sequence 1109, Application US/09827998
APPLICANT: Shannon, Mark
TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
FILE REPERENCE: MDIMORF-8
CURRENT APPLICATION NUMBER: US/09/827,998
CURRENT APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2001-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 1881
SOFTWARE: Acomica Sequence Listing Engine
SEQ ID NO 1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: G. YIZHONG
APPLICANT: G. YIZHONG
APPLICANT: Shannon, Mark
APPLICANT: Shannon, Mark
APPLICANT: Shannon, Mark
TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
FILE REPERENCE: MDHMORF-8
CURRENT APPLICATION NUMBER: US/09/827,998
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/206-26
PRIOR PILING DATE: 2000-09-27
NUMBER OF EQ ID NOS: 1881
SOFTWARE: Aeomica Sequence Listing Engine.
SED ID NO 1110
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                                                                               Query Match 100.0%; Score 10; DB 10; Length 25; Best Local Similarity 100.0%; Pred. No. 1.6e+04; Matches 10; Conservative 0; Mismatches 0; Indels
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larity 100.0%; Pred. No. 1.6e+04;
Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 10; Conservative
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            ; ORGANISM: Homo sapiens US-09-827-998-1108
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US-09-827-998-1109
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US-09-827-998-1110
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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Fatent No. US20020102252A1

GENERAL INFORMATION:
APPLICANT: GL, Yizhong

APPLICANT: Shannon, Mark

TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
FILE REFERENCE: MDHAGNE: US/09/827,998

CURRENT APPLICATION NUMBER: US/09/827,998

CURRENT FILING DATE: 2000-04-06

PRIOR APPLICATION NUMBER: US 60/226

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR APPLICATION SEQUENCE Listing Engine

SOFTWARE: Acomica Sequence Listing Engine
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Fatent No. US20020102252A1

FATENT INFORMATION:

APPLICANT: Shannon, Mark

TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E

FILE REFERENCE: MDHMORF-8

CURRENT APPLICATION NUMBER: US/09/827,998

CURRENT FILING DATE: 2001-04-06

FRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-09-27

NUMBER OF SEQ ID NOS: 1881

SOUTWARE: Asomica Sequence Listing Engine

SEQ ID NO 1108

LENGTH: 25
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 1881
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 1106
LENGTH: 25
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; ORGANISM: Homo sapiens
US-09-827-998-1106
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US-09-827-998-1107
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US-09-827-998-1107/c
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Sequence 1114, Application US/09827998
Fatent No. US200201025221
Fatent No. US200201025221
FAPPLICANT: Gu, Yizhong
APPLICANT: Gu, Yizhong
APPLICANT: Shamon, Mark
ITILE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
CURRENT APPLICATION NUMBER: US/09/827,998
CURRENT FILING DATE: 2001-04-06
FRIOR APPLICATION NUMBER: US 60/207,456
FRIOR APPLICATION NUMBER: US 60/206,359
FRIOR APPLICATION NUMBER: US 60/206,356
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Patent No. US20020102252A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GL, Yizhong
APPLICANT: Shannon, Mark
ITILE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
FILE REPERENCE: MODHORF-8
CURRENT APPLICATION NUMBER: US/09/827, 998 ·
PRIOR PLILNG DATE: 2001-04-06
PRIOR PLILNG DATE: 2000-05-26
PRIOR PLILNG DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
APPLICANT: Shannon, Mark
TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN:
FILE REFERENCE: MDMORFE:
CURRENT EXATION NUMBER: US/09/827,998
CURRENT FILING DATE: 2001-04-06
PRIOR PLLING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 1881
SSOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 1113
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1.6e+04;
thes 0;
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Local Similarity 100...
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                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-1113
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Best Local Similarity
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Patent No. US20020102252A1

GRENERAL INPORMATION:
APPLICANT: Giv, Yizhong
APPLICANT: Shannon, Mark
TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
FILE REPERENCE: MDANORF-8
CURRENT APPLICATION NUMBER: US/09/827,998
CURRENT APPLICATION NUMBER: US/09/827,998
FRIOR APPLICATION NUMBER: US/06/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 1881
SCOFTWARE: Acomica Sequence Listing Engine
SEQ ID NO 1112
LENGTH: 25
                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Gu, Yizhong
APPLICANT: Shannon, Mark
FILLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
FILLE REFERENCE: MDhMORF-8
CURRENT APPLICATION NUMBER: US,009/827,998
CURRENT APPLICATION NUMBER: US,60/207,456
PRIOR PRILING DATE: 2000-05-26
PRIOR PRILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 1881
SOFTWARE APOMICA Sequence Listing Engine
SOFTWARE APOMICA: 25000-09-27
LENGTH: 25
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100.0%; Pred. No. 1.6e+04;
tive 0; Mismatches 0;
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Patent No. US20020102252A1
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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; ORGANISM: Homo sapiens
US-09-827-998-1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
17 CITCICITIT
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US-09-827-998-1113/c
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Sequence 3117, Application US/10060756A

| Bublication No. US20030046717A1
| GENERAL INCPORMATION:
| APPLICANT: Zhang, Jian
| TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
| FILE REPREBNCE: PB0177
| CURRENT APPLICATION NUMBER: US/10/0667 |
| PRIOR APPLICATION NUMBER: PCT/US01/00667 |
| PRIOR APPLICATION NUMBER: PCT/US01/00664 |
| PRIOR APPLICATION NUMBER: PCT/US01/00669 |
| PRIOR PILING DATE: 2001-01-30 |
| PRIOR PLING DATE: 2001-01-30 |
| PRIOR PLING DATE: 2001-01-30 |
| PRIOR FILING DATE: 2001-01-30 |
| PRIOR PRIOR DATE: 200
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; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICATION NO. US20030046717A1
; APPLICATION NO. USZ0030046717A1
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: P80177
; CURRENT APPLICATION NUMBER: US/10/660,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR PILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR PLILING DATE: 2001-01-30
; PRIOR PLILING DATE: 2001-01-30
; PRIOR PLILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR PLILING DATE: 2001-01-30
; PRIOR PLILING DATE: 2001-01-30
; PRIOR PLILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
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                                                              Indels
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                           Pred. No. 1.6e+04;
Mismatches 0;
100.0%; Pre
                        Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                        1 CTTCTCTTT 10
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                                                                                                                                                                                                                                                                                          RESULT 43
US-10-060-756A-3717/c
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US-10-060-756A-3718/c
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LENGTH: 25
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Patent NO. US20020102252A1

GENERAL INFORMATION:
APPLICANT: GL, Yizhong
APPLICANT: GL, Yizhong
APPLICANT: Shannon, Mark
ITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PRECNANCY-ASSOCIATED PROTEIN E
FILE REPERENCE: MDBMORF-8
CURRENT APPLICATION NUMBER: US/09/827,998
CURRENT APPLICATION NUMBER: US/09/827,998
PRIOR APPLICATION NUMBER: US/06/207,456
PRIOR APPLICATION NUMBER: US/06/236,359
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 1881
SOFFWARE APOMICATION SEQ ID NOS: 1881
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APPLICANT: Shadnon, Mark

APPLICANT: Shadnon, Mark

TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E

FILE REFERENCE: MDhMORF-8

CURRENT FILING DATE: 2001-04-06

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

NUMBER OF SEQ ID NOS: 1881

SOFTWARE: Aeomica Sequence Listing Engine

SEQ ID NO 1117

LENGTH: 25
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100.0%; Score 10; DB 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 10; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 1.6e+04;
ative 0; Mismatches 0;
          NUMBER OF SEQ ID NOS: 1881
SOFTWARE: Acomica Sequence Listing Engine
SEQ ID NO 1115
LENGTH: 25
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Best Local Similarity 100.
Matches 10; Conservative
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US-09-827-998-1115
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US-09-827-998-1117
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LENGTH: 25
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| Publication No. US20030046717A1
| GENERAL INPORMATION:
| APPLICANT: Zhang, Jian
| TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
| FILE REPRENCE: PB0177
| CURRENT APPLICATION NUMBER: US/10/066/756A
| CURRENT FILING DATE: 2002-01-30
| PRIOR APPLICATION NUMBER: PCT/US01/00664
| PRIOR FILING DATE: 2001-01-30
| PRIOR APPLICATION NUMBER: PCT/US01/00669
| PRIOR PRILING DATE: 2001-01-30
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100.0%; Pred. No. 1.6e+04;
tive 0; Mismatches 0;
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100.0%; Pred. No. 1.6e+04;
live 0; Mismatches 0;
                                          PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-05-23
PRIOR PRILING DATE: 2001-05-33
PRIOR PRILING DATE: 2001-05-33
PRIOR PRILING DATE: 2001-05-33
PRIOR PRILING DATE: 2001-10-09
NUMBER OF SEQ ID NOS: 4804
SOFTWARE: Aeomica Sequence Listing Engine
SERNGTH: 25
                      NT FILING DATE: 2002-01-30
APPLICATION NUMBER: PCT/US01/00667
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Best Local Similarity 100.
Matches 10; Conservative
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Matches 10, Conservative
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US-10-060-756A-3721
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Publication No. US20030046717A1

GENERAL INFORMATION:

APPLICANT: Zhang, Jian

TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
FILE REFRENCE: PB0177

CURRENT APPLICATION NUMBER: US/10/060,756A

CURRENT FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR PLING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30
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Sequence 3720, Application US/10060756A
Publication No. US20030046717A1
GENERAL INFORMATION:
APPLICANT: Zhang, Jian
ITILE OF INVENTION:
FILE REFERENCE: PB0177
CURRENT APPLICATION NUMBER: US/10/060,756A
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PRIOR APPLICATION NUMBER: US 09/864,761
PRIOR FILING DATE: 2001-05-23
PRIOR PLING DATE: 2001-10-09
NUMBER OF SEQ ID NOS: 4804
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 3718
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Best Local Similarity 100.
Matches 10; Conservative
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ORGANISM: Homo sapiens
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US-10-060-756A-3719
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Best Local Similarity
Matches 10; Conserv
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US-10-060-756A-3724/C

Sequence 3724 Application US/10060756A

Publication No. US20030046717A1

GENERAL INFORMATION:

APPLICANT: Zhang, Jian

TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN

FILE REFERENCE: BRO177

CURRENT APPLICATION NUMBER: US/10/060,756A

CURRENT APPLICATION NUMBER: PCT/US01/00667

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30
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CHDication No. US20030046717A1
GENERAL INFORMATION.
APPLICANT: Zhang, Jian
TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
CURRENT APPLICATION UNDER: US/10/660,756A
CURRENT FILING DATE: 2002-01-30
PRIOR PAPLICATION NUMBER: PCT/US01/00667
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
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       NUMBER OF SEQ ID NOS: 4804
SOFTWARE: Acomica Sequence Listing Engine
SEQ ID NO 3723
LENGTH: 25
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                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                            TYPE: DNA
CORGANISM: Homo sapiens
US-10-060-756A-3723
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ORGANISM: Homo sapiens
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US-10-060-756A-3725/c
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TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
FILE REFERENCE: PB0177

CURRENT APPLICATION NUMBER: US/10/066,756A

CURRENT FILING DATE: 2002-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR PILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR PELING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR PLING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-10-09

NUMBER OF SEQ ID NOS: 4804

SOPTWARE: Aeomica Sequence Listing Engine

SEQ ID NO 3722

LENGTH: 25
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Publication No. US20030046717A1

GENERAL INFORMATION:

FILE REPERENCALINGUE

CURRENT APPLICATION HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN

FILE REPERENCE: PB0177

CURRENT APPLICATION NUMBER: US/10/060,756A

CURRENT FILING DATE: 2002-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30
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Sequence 3722, Application US/10060756A
Fublication No. US20030046717A1
GENERAL INFORMATION:
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21 CTTCTCTTT 12
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Matches 10; Conserv
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US-10-060-756A-3723/c
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Sequence 3727, Aprication US/10060756A
| Publication No US20030046717A1
| GENERAL INROPARTION:
| APPLICAMT: Zhang, Jian
| TILE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
| FILE REFRENCE: PB0.17
| CURRENT APPLICATION NUMBER: US/10/066,756A
| CURRENT PILING DATE: 2002-01-30
| PRIOR PILING DATE: 2001-01-30
| PRIOR APPLICATION NUMBER: PCT/US01/00667
| PRIOR APPLICATION NUMBER: PCT/US01/00669
| PRIOR FILING DATE: 2001-01-30
| PRIOR FILING DATE: 2001-01-30
| PRIOR PILING DATE: 2001-01-30
| PRIOR PILING DATE: 2001-01-30
| PRIOR APPLICATION NUMBER: PCT/US01/00668
| PRIOR FILING DATE: 2001-01-30
| PRIOR APPLICATION NUMBER: PCT/US01/00668
| PRIOR FILING DATE: 2001-01-30
| PRIOR APPLICATION NUMBER: PCT/US01/00668
| PRIOR FILING DATE: 2001-01-30
| PRIOR PILING DATE: 2001-01-30
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| Publication No US20030046717A1
| GENERAL INFORMATION:
| APPLICANT: Zhang, Jian
| TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
| FILE REFREENCE: PB0177
| CURRENT APPLICATION NUMBER: US/10/066/756A
| CURRENT FILING DATE: 2002-01-30
| PRIOR APPLICATION NUMBER: PCT/US01/00664
| PRIOR PILING DATE: 2001-01-30
| PRIOR PLICATION NUMBER: PCT/US01/00669
| PRIOR PLICATION NUMBER: PCT/US01/00669
| PRIOR PLICATION NUMBER: PCT/US01/00665
| PRIOR PLILING DATE: 2001-01-30
| PRIOR PLILING DATE: 2001-00-30
| PRIOR PLILING DATE: 2001-01-30
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Best Local Similarity 100.
Matches 10, Conservative
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US-10-060-756A-3728/c
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Sequence 3726, 4pplication US/10060756A

Publication No. US20030046717A1

GENERAL INFORMATION:

APPLICANT: Zhang, Jian

TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN

FILE REFERENCE: PB0177

CURRENT APPLICATION NUMBER: US/10/066, 756A

CURRENT FILING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

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PRIOR PLING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR PLING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/327,898

PRIOR PLING DATE: 2001-05-3

PRIOR APPLICATION NUMBER: US 60/327,898

PRIOR APPLICATION NUMBER: US 60/327,898
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-05-23
PRIOR FILING DATE: 2001-05-23
PRIOR FILING DATE: 2001-05-23
PRIOR FILING DATE: 2001-05-33
PRIOR FILING DATE: 2001-06-63
PRIOR FILING DATE: 2001-06-63
PRIOR FILING DATE: 2001-06-9
PRIOR PILING DATE: 2001-06-9
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; ORGANISM: Homo sapiens
US-10-060-756A-3725
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ORGANISM: Homo sapiens
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## APPLICANT: Zhang, Jian

## APPLICANT: Zhang, Jian

## TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN

## REPERENCE: PBO177

**CURRENT APPLICATION NUMBER: US/10/066,756A

**CURRENT FILING DATE: 2002-01-30

**PRIOR APPLICATION NUMBER: PCT/US01/00664

**PRIOR PELING DATE: 2001-01-30

**PRIOR APPLICATION NUMBER: PCT/US01/00669

**PRIOR PILING DATE: 2001-01-30

**PRIOR APPLICATION NUMBER: PCT/US01/00668

**PRIOR FILING DATE: 2001-01-30

**PRIOR PELING DATE: 2001-05-23

**PRIOR PELING DATE: 2001-05-23

**PRIOR PELING DATE: 2001-05-33

**PRIOR PELING DATE: 2001-05-33

**PRIOR PELING DATE: 2001-05-33

**PRIOR APPLICATION NUMBER: US 60/327, 898

**PRIOR APPLICATION UMBER: US 60/327, 898

**PRIOR APPLICA
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100.0%; Pred. No. 1.6e+04;
tive 0; Mismatches 0;
                                         PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-05-23
PRIOR FILING DATE: 2001-05-23
PRIOR FILING DATE: 2001-05-23
PRIOR FILING DATE: 2001-05-39
PRIOR FILING DATE: 2001-05-39
PRIOR FILING DATE: 2001-05-3
NUMBER OF SEQ ID NOS: 4804
SOFTWARE: Acomica Sequence Listing Engine
SEQ ID NO 3730
                    FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3731, Application US/10060756A Publication No. US20030046717A1 GENERAL INFORMATION:
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US-10-060-756A-3732/c
; Sequence 3732, Application US/10060756A
; Publication No. US20030046717A1
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
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; ORGANISM: Homo sapiens
US-10-060-756A-3730
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ORGANISM: Homo sapiens
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APPLICANT: Zhang, Jian

TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
FILE REPERENCE: PB0177

CURRENT APPLICATION NUMBER: US/10/060,756A

CURRENT FILING DATE: 2002-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PPLING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR PPLING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR PPLING DATE: 2001-01-30

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TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
FILE REFERENCE: PB0177
                                                                                                                                                             Query Match
100.0%; Score 10; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 10; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.6e+04;
ative 0; Mismatches 0;
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CURRENT FILING DATE: 2002-01-30
PRIOR PAPLICATION NUMBER: PCT/US01/00667
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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Sequence 3729, Application US/10060756A
Publication No. US20030046717A1
GENERAL INFORMATION:
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; TYPE: DNA; ORGANISM: Homo sapiens US-10-060-756A-3728
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Best Local Similarity
Matches 10; Conserv
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| Publication No. US20030104410A1
| GENERAL INFORMATION:
| APPLICANT: Mitthen, Michael
| TITLE OF INVENTION: Human Microarray
| FILE REPRENCE: 3118.1
| CURRENT APPLICATION NUMBER: US/10/098,263B
| CURRENT FILING DATE: 2003-01-08
| PRIOR FILING DATE: 2001-03-16
| NUMBER OF SEQ ID NOS: 131066
| NUMBER OF SEQ ID NOS: 131066
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Sequence 7372, Application US/10215112

Sequence 7372, Application US/10215112

Bublication No. US20030082596A1

GENERAL INFORMATION:

APPLICANT: Michael Mittmann

TITLE OF INVENTION: Test3

FILE REFERENCE: 3119

CURRENT APPLICATION NUMBER: US/10/215,112

CURRENT APPLICATION NUMBER: 2002-08-08

NUMBER OF SEQ ID NOS: 14936

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 25
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                APPLICANT: Michael Mittmann
TITLE OF INVENTION: Method of Genetic Analysis of Probes:
TITLE OF INVENTION: Test3
FILE REFERENCE: 3119
CURRENT APPLICATION NUMBER: US/10/215,112
CURRENT FILING DATE: 2002-08
NUMBER OF SEQ ID NOS: 14936
SEQ ID NOS: 14936
SEQ ID NOS: 1250
LENGTH: 25
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Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 10; Conservative 0; Mismatches 0;
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100.0%; Score 10; DB 14;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 10; Conservative 0; Mismatches 0:
                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Synthetic Oligonucleotide US-10-215-112-7250
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US-10-098-263B-6553
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LENGTH: 25
TYPE: DNA
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TILE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
FILE REFERENCE: PB0177
CURRENT APPLICATION NUMBER: US/10/060,756A
CURRENT FILING DATE: 2002-01-30
PRIOR PELICATION NUMBER: PCT/US01/00667
PRIOR PELICATION NUMBER: PCT/US01/00664
PRIOR PELICATION NUMBER: PCT/US01/00669
PRIOR PELICATION NUMBER: PCT/US01/00669
PRIOR PILING DATE: 2001-01-30
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Sequence 7249, Application US/10215112

Sequence 7249, Application US/10215112

Publication No. US20030082596A1

GENERAL INFORMATION:

APPLICANT: Michael Mittmann

TITLE OF INVENTION: Test3

FILE REFERENCE: 3119

CURRENT APPLICATION UNDBER: US/10/215,112

CURRENT FILING DATE: 2002-08-08

NUMBER OF SEQ ID NOS: 14936

SEQ ID NO 7249

LENGTH: 25
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100.0%; Pred. No. 1.6e+04;
tive 0; Mismatches 0;
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SOFTWARE: Acomica Sequence Listing Engine
SEQ ID NO 3132
LENGTH: 25
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8-10-210-112-7250/c
; Sequence 7250, Application US/10215112
; Publication No. US20030082596A1
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Matches 10, Conservative
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ORGANISM: Homo sapiens
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Sequence 86720, Application US/10098263B; Publication No. US20031014410A1; GENERAL INVORMATION:
GENERAL INVORMATION:
TITLE OF INVENTION: Human Microarray; FILE REFERENCE: 3118.1
CURRENT FILING DATE: 2003-01-08; PRIOR FILING DATE: 2003-01-08; PRIOR FILING DATE: 2001-01-06; NUMBER OF SEQ ID NOS: 131066; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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Sequence 114427, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 05/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 114427
LENGTH: 25
TENGTH: 25
TENGTH: 25
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                                         APPLICANT: Mitthan, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 31181
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION UNMBER: 60/276,759
PRIOR PILING DATE: 2001-316
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 10; DB 14; 100.0%; Pred. No. 1.6e+04;
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      Publication No. US20030104410A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 10, Conservative
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapien
US-10-098-263B-41737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-86720
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ORGANISM: Homo sapien
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US-10-098-263B-86720/c
                                                                                                                                                                                                                                                   SEQ ID NO 41737
LENGTH: 25
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Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Mitthen, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
FRIOR APPLICATION NUMBER: 60/276,759
FRIOR APPLICATION NUMBER: 60/276,759
FRIOR APPLICATION NUMBER: 5001-03-16
NUMBER OF SEC ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
TEMPORAL OF 100 10333
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Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Mitchean, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION WUMBER: US/10/098,263B
CURRENT APPLICATION WUMBER: 60/276,759
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
                                                            100.0%; Score 10; DB 14; Length 25; 100.0%; Pred. No. 1.6e+04; Live 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 10; Conservative
                                                                                   Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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; ORGANISM: Homo sapien
US-10-098-263B-6553
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; ORGANISM: Homo sapien
US-10-098-263B-10333
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US-10-098-263B-34049
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US-10-098-263B-10333
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                                                                 Query Match
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Gaps

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Query Match
Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-118058
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ORGANISM: Homo sapien
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US-10-098-263B-118243
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Sequence 114421, Application US/10098263B

Publication No. US2030104410A1

GENERAL INFORMATION:

APPLICANT: Mitthan, Michael

FILE REFERENCE: 3118.1

FULR REPERENCE: 3118.1

CURRENT FILING DATE: 2003-01-08

PRIOR APPLICATION NUMBER: 60/276,759

PRIOR APPLICATION NUMBER: 60/276,759

PRIOR PELLING DATE: 2001-03.16

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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Sequence 118057, Application US/10098263B
Sequence 118057, Application US/10098263B
Sequence 118057, Application US/10098263B
SEQUENCE INFORMATION: Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 318.4
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT APPLICATION NUMBER: US/10/098
FRIOR FILING DATE: 2003-01-08
FRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
                                        Length 25
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                                  100.0%; Score 10; DB 14;
100.0%; Pred. No. 1.6e+04;
                                                                       0; Mismatches
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US-10-098-263B-118058
; Sequence 118058, Application US/10098263B
; Publication No. US20030104410A1
                               Query Match
Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                        1 CTICICITIE 10
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ORGANISM: Homo sapien
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; ORGANISM: Homo sapien
US-10-098-263B-118057
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Best Local Similarity
Matches 10; Conserv
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US-10-098-263B-114427
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US-10-098-263B-114428
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US-10-098-263B-118057
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Fublication No. US20030104410A1
GENERAL INFORMATION:
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
FRIGH FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
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Fublication No. US20030104410A1
GENERAL INFORMATION:
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2003-01-08
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                             Length 25;
APPLICANT MITTER, Mitchael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 31181.
FILE REPERENCE: 31181.
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 118058
LENGTH: 25
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100.0%; Score 10; DB 14;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 10; Conservative 0; Mismatches 0;
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; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-780-533A-2783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2783, Application US/09780533A
| Publication No. US20030060611A1 |
| GENERAL INFORMATION |
| APPLICANT: Ribozyme Pharmaceuticals, Inc. |
| APPLICANT: Blatt, Larry |
| APPLICANT: McSwiggen, Jim |
| APPLICANT: McSwiggen, Jim |
| APPLICANT: McSwiggen, Jim |
| APPLICANT: Haeberli, Pete |
| TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene |
| TITLE OF INVENTION: Method and A (400/011) |
| CURRENT APPLICATION NUMBER: US/09/780,533A |
| CURRENT APPLICATION NUMBER: US 60/181,797 |
| PRIOR PILING DATE: 2000-02-11 |
| NUMBER OF SED ID NOS: 6679 |
| SOFTWARE: PatentIn version 3.0 |
| LINGTH: 38 |
| LINGTH: 38
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APPLICANT: Blatt, Larry
APPLICANT: Chowitian, Dim
APPLICANT: Chowitian, Dharat
APPLICANT: Chowitian, Dear
APPLICANT: Haeberli, Peter
ITILE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
FILE REPERBNCE: MBHB00,878 A (400/011)
CURRENT APPLICATION NUMBER: US 60/181,797
PRIOR APPLICATION NUMBER: US 60/181,797
PRIOR PILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 6679
SOFTWARE: Patentin version 3.0
SEQ ID NO 4693
LENGTH: 38
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100.0%; Pred. No. 1.5e+04;
Live 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 10; Conservative 0; Mismatches 0;
                                                                                                                          TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 359:
US-09-765-272-359
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GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
INFORMATION FOR SEQ ID NO: 359:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
                                                                             TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 10; Conservative
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TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SQUENCES: 452
CORRESPONDENCE ADDRESS: 452
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                          Gaps
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) Publication No. US20030104410A1
GENERAL INFORMATION:
) APPLICANT: Mittenan, Michael
) TITLE OF INVENTION: Human Microarray
) FILE REFERENCE: 3118.1
) CURRENT APPLICATION NUMBER: US/10/098,263B
) PRIOR APPLICATION NUMBER: 60/276,759
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR PELLING DATE: 2001-03-16
) NUMBER OF SEQ ID NOS: 131066
) SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
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COMPUTER READABLE FORM:
MEDIUM TEBED EDISACTE, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDGS version 6.2
SOFTWARE: ASCII Pext
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,272
FILING DATE: 22-Jan-2001
CLASSIPICATION: -CURMOWN->
PRIOR APPLICATION: AUKHOWN->
APPLICATION DATA:
APPLICATION OF AUKHOWN->
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APPLICATION OF AUKHOWN->
APPLICATION OF AUKHOWN->
                           Length 25;
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                                                                        0; Indels
                   100.0%; Score 10; DB 14;
100.0%; Pred. No. 1.6e+04;
tive 0; Mismatches 0;
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REGISTRATION NUMBER: 36,373
REPERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 359, Application US/09765272
Patent No. US20020061545A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 10; Conservative
                                                                   10; Conservative
                                                                                                                                         15 CTTCTCTTT 24
                                                                                                                  1 CTTCTCTTT 10
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ORGANISM: Homo sapien
                                          Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                  RESULT 73
US-10-098-263B-119613
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                      Query Match
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APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Variable APPLICANT: Jarvis, Thale
APPLICANT: Van Carlowitz, Ira
APPLICANT: Won Carlowitz, Ira
APPLICANT: McSwiggen, Jim
APPLICANT: Hamblin, Paul
APPLICANT: Hamblin, Paul
APPLICANT: Ellis, Jonathan
ATTLE OF INVENTION: McHood and Reagent for the Inhibition of Grb-2-related with Inse
TITLE OF INVENTION: (GRID) Gene
FILE REFERENCE: MBHB00-901-A (400/013)
CURRENT APPLICATION NUMBER: US/09/792,818
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 2304
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-792-818-944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lo. Donald C.
APPLICANT: Barney, Shawn
APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Thomas, Mary Beth
APPLICANT: Puranam, Kasturi
APPLICANT: Puranam, Kasturi
APPLICANT: Puranam, Kasturi
APPLICANT: War Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: CELL DEATH
FILE REPRENCE: 10001-065-999
CURRENT APPLICATION NUMBER: US/09/922,261
CURRENT FILING DATE: 108-03
PRIOR APPLICATION NUMBER: US/09/461,697
WINNERS OF DATE: 108-09-12-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 10; DB 12; Length 38; Best Local Similarity 100.0%; Pred. No. 1.5e+04; Matches 10; Conservative 0; Mismatches 0; Indels
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; Score 10; DB 11; Length 38; Pred. No. 1.5e+04; 7; Mismatches 0; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                        ; Sequence 944, Application US/09792818; Publication No. US20030134806A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 227, Application US/09922261
Patent No. US20020111471A1
GENERAL INFORMATION:
APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: Lo, Donald C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                    30.08;
Query Match
Best Local Similarity 30.03
Matches 3; Conservative
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                                                                                                                                                                                               RESULT 78
US-09-792-818-944/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-922-261-227/c
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LENGTH: 42
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NAME/KEY: misc_feature
LOCATION: (11)..(16)
OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
NAME/KEY: misc_feature
LOCATION: (20)..(20)
OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
NAME/KEY: misc feature
LOCATION: (22)..(22)
OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
NAME/KEY: misc feature
LOCATION: (22)..(25)
OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
NAME/KEY: misc feature
LOCATION: (24)..(25)
                      ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-780-533A-4693
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                                                                                                                                                                               Gaps
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OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
                                                                                                                             100.0%; Score 10; DB 11; Length 38; 30.0%; Pred. No. 1.5e+04; Live 7; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                     Sequence 4478, Application US/09877478
Publication No. US20030068301A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                             Query Match
Best Local Similarity 30.09
Matches 3; Conservative
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29 cuucucuuuu 38
                                                                                                                                                                                                                        1 CTICICITIT 10
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LENGTH: 38
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Gaps .; 0

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US-09-997-931-40/c

Sequence 40, Application US/09997931

Publication No. US2030087241A1

GENERAL INFORMATION:
APPLICANT: University of Rochester
TILE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND DNA
FILE REFERENCE: 220.0010142
CURRENT APPLICATION NUMBER: US/09/997,931
CURRENT APPLICATION NUMBER: US/09/997,931

PRIOR FILING DATE: 2000-05-11
PRIOR FILING DATE: 1997-02-26
PRIOR FILING DATE: 1997-02-26
PRIOR FILING DATE: 1995-02-23
PRIOR FILING DATE: 1995-02-23
PRIOR FILING DATE: 1993-04-15
NUMBER OF SEQ ID NOS: 129
SOFTWARE PATENTING DATE: 1993-04-15
NUMBER OF SEQ ID NOS: 129
SOFTWARE PATENTING DATE: 1993-04-15
NUMBER OF SEQ ID NOS: 129
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Sequence 41, Application US/09997931

Publication No. US20303087241A1

GENERAL INFORMATION:
APPLICANT: University of Rochester
APPLICANT: University of Rochester
APPLICANT: University of Rochester
TITLE OF INVENTION: Eric
TITLE OF INVENTION: Eric
CURRENT FELING DATE: 200.101-30

PRIOR APPLICATION NUMBER: US/09/997,931

CURRENT FILING DATE: 2000-05-11

PRIOR PELICATION NUMBER: US 08/569,344

PRIOR PELICATION NUMBER: US 08/393,439

PRIOR FILING DATE: 1997-02-26

PRIOR APPLICATION NUMBER: US 08/393,439

PRIOR PLICATION NUMBER: US 08/393,439

PRIOR PLICATION NUMBER: US 08/47,860

PRIOR PLILING DATE: 1993-04-15

NUMBER OF SEQ ID NOS: 129

SEQ ID NO 41

LEMETH: 53

LEMETH: 53

LEMETH: 53
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OTHER INFORMATION: stem-loop multimer which binds HIV-1 gag RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 10; Conservative 0; Mismatches 0; Indels
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100.0%; Score 10; DB 11; Length 53;
Best Local Similarity 30.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 7; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTCTCTTT 16
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Patent No. US20020111471A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lo, Donald C.
APPLICANT: Lo, Donald C.
APPLICANT: Barney, Shawn
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Matz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: COMPOSITIONS AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
FILLE REFERENCE: L0001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
PRIOR APPLICANTON NUMBER: US/09/461,697
PRIOR FILLING DATE: 2001-08-03
PRIOR FILLING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FREESEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                              APPLICANT: Terry, Roemer D.
APPLICANT: Terry, Roemer D.
APPLICANT: Bo, Jiang
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1923
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Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 10; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.5e+04;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                               Sequence 1923, Application US/10032585
Publication No. US20030180953A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
CORGANISM: Candida albicans
US-10-032-585-1923
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
                                                                              1 CITCICITII 10
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LENGTH: 48
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Sequence 31961/c

Sequence 31961, Application US/09908975

Sequence 31961, Application US/09908975

Sequence 31961, Application No. US20030165843A1

Sequence 31961, Application No. US20030165843A1

APPLICANT: SHOSHAN, Avi

APPLICANT: MASSERMAN, Alon

TITLE OF INVENTION: DIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE

TITLE OF INVENTION: ULGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE

TITLE OF INVENTION: UNMBER: US/09/908,975

CURRENT APPLICATION NUMBER: US 60/287,724

PRIOR PPLICATION NUMBER: US 60/287,724

PRIOR PELLING DATE: 2001-05-02

PRIOR APPLICATION NUMBER: US 60/221,607

PRIOR SEQ ID NOS: 32337

SOFTWARE: PALENTIN VERSION 3.0
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Fatent No. US2002045577A1
GENERAL INFORMATION:
APPLICANT: Stefansson, Hreinn
APPLICANT: Stefansson, Hreinn
APPLICANT: Stefanson, HUMAN SCHIZOPHRENIA
FILE REPERBENCE: 2345.2004.001
CURRENT FILING DATE: 2001-02-28
CURRENT PELING DATE: 2000-02-28
FRIOR APPLICATION NUMBER: US/09/55,668
CURRENT FILING DATE: 2000-02-28
FRIOR PELICATION NUMBER: US/09/515,716
FRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 1531
SOSTWARE: FARESEQ for Windows Version 4.0
SEQ ID NO 1332
LENGTH: 61
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43 CTTCTCTTTT 52
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US-09-908-975-31961
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US-09-795-668-1332
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US-09-795-686-1332
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LENGTH: 60
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Sequence 18382, Application US/09908975

Sequence 18382, Application US/09908975

Publication No. US20030165843A1

SENERAL INPORMATION:
APPLICANT: SHOSHRAN, Avi
APPLICANT: MINTZ, Liat
APPL
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US-10-085-906-282

y Sequence 202, Application US/10085906
y Publication No. US20030054371A1
GREBAL INFORMATION:
APPLICANT: Wu, Paul
APPLICANT: Wu, Paul
TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
TITLE OF INVENTION: COSTUMICATOR RECEPTOR LOCUS AND USES THEREOF
FILE REFERENCE: GNN -5343CP2
CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: US 60/126,215
PRIOR APPLICATION NUMBER: US 60/126,215
PRIOR APPLICATION NUMBER: PCT/US00/07938
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 545
NUMBER OF SEQ ID NOS: 545
LENGTH: 59
LENGTH: 59
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SOFTWARE: Patentin version 3.0
SEQ ID NO 18382
LENGTH: 60
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Best Local Similarity 100.(
Matches 10, Conservative
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38 CUUCUCUUUU 47
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       1 CTTCTCTTT 10
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US-09-908-975-18382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-906-282
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1 CTTCTCTTT 10

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Sequence 5096, Application US/09983965
; Sequence 5096, Application US/09983965
; Patent No. US20020137160A1
; GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: MUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REFERENCE: 37-21(10297)C
CURRENT APPLICATION NUMBER: US/09/983,965
CURRENT PILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 5912
; SEQ ID NO 5096
; TEMBER OF SEQ ID NOS: 5912
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US-09-983-965-5096
                PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR PLING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-03-28
PRIOR FILING DATE: 1999-03-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1099-08-09
PRIOR FILING DATE: 1099-08-
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Sequence 276, Application US/10085906
Publication No. US20030054371A1
GENERAL INFORMATION:
APPLICANT: Ying, Vincent
APPLICANT: Wu, Paul
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Best Local Similarity 100...
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-027-632-58348
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GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFRENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
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100.0%; Pred. No. 1.4e+04;
iive 0; Mismatches 0;
Sequence 1332, Application US/09795686
Patent No. US20020094954a1
GENERAL INFORMATION:
APPLICANT: Stefansson, Hreinn
APPLICANT: Stefansson, Hreinn
APPLICANT: Gulcher, Jeffrey, R.
ITLLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE FEFRENT GALCHER: 2345,2005-001
CURRENT APPLICATION NUMBER: US/09/795,686
CURRENT APPLICATION NUMBER: US 09/515,715
PRIOR PILING DATE: 2001-02-28
FRIOR APPLICATION NUMBER: US 09/515,715
PRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 1531
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1332, Application US/09946807
Patent No. US20020165144A1
GENERAL INFORMATION:
APPLICANT: Stefansson, Hreinn
APPLICANT: Steinthorsdottir, Valgerdur
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2004-001
CURRENT FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: US/09/795,668
PRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ 1D NOS: 1531
SOFTWARE: FastSEG for Windows Version 4.0
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-795-686-1332
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US-09-946-807-1332
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US-10-027-632-58348
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US-09-946-807-1332
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APPLICANT: FAIGLER, Simchon

TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICITIES OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICITIES OF INVENTION: THAT POPULATE A TRANSCRIPTOME
FILE REFERENCE: 36689-0005
CURRENT APPLICATION NUMBER: US (09/908,975
CURRENT PILING DATE: 2001-07-20
PRIOR PILING DATE: 2001-05-02
PRIOR PILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: PARENT SOURCE SOURCE SEQ ID NOS: 32337
SOFTWARE: PARENT SACRET SOURCE SEQ ID NOS: 32037
LENGTH: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 95
US-10-012-585-135
US-10-012-585-135
Sequence 135, Application US/10032585
Fublication No. US20030180953A1
GENERAL INFORMATION:
APPLICANT: Terry, Roemer D.
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussel
APPLICANT
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Publication No. US20030180953A1
GENERAL INFORMATION:
APPLICANT: Terry, Roemer D.
APPLICANT: Howard Bussey
APPLICANT: Howard Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT PILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 10; DB 12; Length 65; 100.0%; Pred. No. 1.4e+04; ttive 0; Mismatches 0; Indels
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ORGANISM: Candida albicans
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Best Local Similarity 100...
Best Local Similarity 100...
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    MINTZ, Liat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-908-975-28061
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        APPLICANT:
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APPLICANT: WASSERMAN, Alon
APPLICANT: WASSERMAN, Alon
APPLICANT: WINTZ, Liat
APPLICANT: WINTZ, Liat
APPLICANT: WINTZ, Liat
APPLICANT: FAIGLER, Simchon
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBERRY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBERRY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
FILE REPERENCE: 3668-005
CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT FILING DATE: 2001-07-20
PRIOR FILING DATE: 2001-05-02
PRIOR FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 32337
SOSTWARE: PATCHIL VETSION 3.0
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APPLICANT: Gray, Gary S.
TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
CURRENT APPLICATION NUMBER: US /01/0685,906
CURRENT APPLICATION NUMBER: US /02/126,215
PRIOR APPLICATION NUMBER: US /05/126,215
PRIOR FILING DATE: 2000-03-24
PRIOR PRILING DATE: 2000-03-24
PRIOR PILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 545
SOFTWARE: FastSEQ for Windows Version 4.0
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100.0%; Score 10; DB 12; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.40+04;
Matches 10; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 27615, Application US/09908975; Publication No. US20030165843A1; GENERAL INFORMATION:
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APPLICANT: WASSERMAN, Alon
APPLICANT: MINTZ, Eli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.'
Matches 10; Conservative
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US-09-908-975-27615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
CORGANISM: Homo sapiens
US-10-085-906-276
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Best Local Similarity 100.
Matches 10; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
         Query Match
Best Local Similarity
Matches 10; Conserv
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US-10-029-386-17114
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APPLICANT: Terry, Roemer D.
APPLICANT: Charles, Boone
APPLICANT: Charles, Boone
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REPRENDE: 10.182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT APPLICATION DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: Patentin version 3.1
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                                                                                                                   Length 65;
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                                                                                                                                                       0; Indels
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APPLICANT: Wang, Qi
APPLICANT: Liang, Jihong
APPLICANT: Liang, Jihong
APPLICANT: Liang, Jihong
TITLE OF INVENTION: Arcelin-5 Promoter and Uses Thereof
FILE REFERENCE: 13587.106
CURRENT APPLICATION NUMBER: US/10/015,637
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: US 60/255879
PRIOR FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
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100.0%; Score 10; DB 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 10; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                   Sequence 2790, Application US/10032585
Publication No. US20030180953A1
GENERAL INFORMATION:
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Publication No. US20030046727A1
GENERAL INFORMATION:
                                  TYPE: DNA
CRGANISM: Candida albicans
US-10-032-585-152
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US-10-032-585-2790
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity
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SEQ ID NO 152
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US-10-015-637-3
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LENGTH: 76
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US-10-029-386-24504

(Sequence 24504, Application US/10029386

(Sequence 24504, Application Wo. US20030194704A1

(SERERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Hanzel, David R.

ITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TILLE OF INVENTION: HUMAN GENOME.

FILE REFERENCE: AECMICA-X-2

CURRENT FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 34288

SOFTWARE: Annomax Sequence Listing Engine vers: 1.1

SEQ ID NO 24504

"ENGINE OF SECTION OF 
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Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REPERBENCE: AEOMICA.X.2
CURRENT APPLICATION UNMERR: US/10/029,386
CURRENT APPLICATION UNMERR: US/10/029,386
CURRENT APPLICATION UNMERR: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
LENGTH: 84
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; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1

; OTHER INFORMATION: EST_HUMAN HIT: AW905636.1, EVALUE 9.00e-02

US-10-029-386-24504
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OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN HELLA, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5

OTHER INFORMATION: EST HUMAN HIT: BES36158.1, EVALUE 9.50e-02

OTHER INFORMATION: NT HIT: X03248.1, EVALUE 1.00e+00
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Search completed: October 28, 2003, 18:49:54 Job time : 1754 secs